

GenCore version 5.1.4 p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 11:56:08 ; Search time 1730.44 Seconds

(without alignments)
4490.451 Million cell updates/sec

Title: US-09-823-101-9

Perfect score: 267
Sequence: 1 acttcacgtctctcagtcctc.....aagagagaaanncnttgat 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_ov: *
5: gb_om: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_ph: *
24: em_pl: *
25: em_ro: *
26: em_sts: *
27: em_vl: *
28: em_vl: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rod: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	263	98.5	267	6	AX338096	AX338096 Sequence
2	131.8	49.4	1051	6	AR164814	AR164814 Sequence
3	131	49.1	168991	2	AC025462	AC025462 Homo sapi
4	128.4	48.1	214139	2	AC022129	AC022129 Homo sapi
5	128	47.9	165563	2	AC083752	AC083752 Mus muscu
6	126	47.2	2319	9	HSMB05518	AL834213 Homo sapi
7	125.2	46.9	3307	10	BC018613	BC018613 Mus muscu
8	124.8	46.7	3353	9	HSMB03622	AL832315 Homo sapi
9	124.8	46.7	162610	2	AC106565	AC106565 Rattus no
10	124.6	46.7	1661	9	BC025755	BC025755 Homo sapi
11	124.6	46.7	133276	2	AC087147	AC087147 Mus muscu
12	124.4	46.6	2975	9	HSMB04650	AL833337 Homo sapi
13	124.2	46.5	2674	6	AR183261	AR183261 Sequence
14	124	46.4	1044	9	AB019565	AB019565 Homo sapi
15	123.4	46.2	169404	2	AC094999	AC094999 Rattus no
16	122.8	46.0	1071	9	AF078844	AF078844 Homo sapi
17	122.8	46.0	1690	9	BC011595	BC011595 Homo sapi
18	122.8	46.0	1694	9	BC012597	BC012597 Homo sapi
19	122.4	45.8	2198	9	HSMB03382	AL832075 Homo sapi
20	122.4	45.8	12007	6	AX345619	AX345619 Sequence
21	122.4	45.8	179206	9	CNS01DS6	AL121656 BAC sequ
22	122.2	45.8	1243	9	HSMB02621	AL162083 Homo sapi
23	122.2	45.8	2096	10	BC034131	BC034131 Mus muscu
24	122.2	45.8	3178	9	HSMB03719	AL832411 Homo sapi
25	122.2	45.8	4043	10	BC020177	BC020177 Mus muscu
26	122	45.7	4962	9	HSMB04543	AL833232 Homo sapi
27	122	45.7	8392	6	AX346392	AX346392 Sequence
28	121.8	45.6	4362	9	HSMB05498	AL834414 Homo sapi
29	121.8	45.6	6719	9	HSMB03507	AL832200 Homo sapi
30	121.6	45.5	144	6	BD005387	BD005387 Secreted
31	121.6	45.5	144	6	189947	189947 Sequence 26
32	121.6	45.5	1652	9	BC028121	BC028121 Homo sapi
33	121.6	45.5	7306	6	AX346539	AX346539 Sequence
34	121.6	45.5	15832	6	AX277943	AX277943 Sequence
35	121.6	45.5	15832	6	AX323630	AX323630 Sequence
36	121.6	45.5	15832	6	AX346245	AX346245 Sequence
37	121.6	45.5	349980	6	AX344551	AX344551 Sequence
38	121.4	45.5	2194	10	BC031202	BC031202 Mus muscu
39	121.4	45.5	2447	9	BC027927	BC027927 Homo sapi
40	121.4	45.5	2747	9	BC025706	BC025706 Homo sapi
41	121.4	45.5	6794	6	AX251872	AX251872 Sequence
42	121.4	45.5	6794	6	AX344260	AX344260 Sequence
43	121.4	45.5	6794	6	AX348651	AX348651 Sequence
44	121.2	45.4	1521	17	AF118070	AF118070 Homo sapi
45	121.2	45.4	2260	17	AF116602	AF116602 Homo sapi

ALIGNMENTS

RESULT 1	AX338096	267 bp	DNA	linear	PAT 09-JAN-2002
LOCUS	AX338096				
DEFINITION	Sequence 9 from Patent WO0175169.				
ACCESSION	AX338096				
VERSION	AX338096.1				
KEYWORDS	GI:18128727				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Pluta, V., Chen, S.-Y., Hu, P., Recipon, H. and Macina, R.A.				
	Compositions and methods for diagnosing, monitoring, staging,				
	imaging and treating stomach cancer				

JOURNAL Patent: WO 01/75169-A 9 11-OCT-2001;
Diadexus, Inc. (US)
FEATURES Location/Qualifiers
Source 1..267
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 147 a 33 c 62 g 21 t 4 others
ORIGIN

Query Match 98.5%; Score 263; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACTTCACCTGCTCAGTCTCTAGAGCCCTGANAATAAACAACCTATTATTCACAGT 60
DB 1 ACTTCACCTGCTCAGTCTCTAGAGCCCTGANAATAAACAACCTATTATTCACAGT 60
OY 61 AA 120
DB 61 AA 120
OY 121 AAGGGGGGG 180
DB 121 AAGGGGGGG 180
OY 181 GGG 240
DB 181 GGG 240
OY 241 AAACAAAAGAGAGAAANNCNTTGAT 267
DB 241 AAACAAAAGAGAGAAANNCNTTGAT 267

RESULT 2
ARI64814
LOCUS ARI64814 1051 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 10 from patent: US 6274339.
ACCESSION ARI64814
VERSION ARI64814.1 GI:16238023
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1051)
AUTHORS Moore, K. and Nagle, D. Lynn.
TITLE Methods and compositions for the diagnosis and treatment of body weight disorders, including obesity
JOURNAL Patent: US 6274339-A 10 14-AUG-2001;
FEATURES Location/Qualifiers
Source 1..1051
/organism="unknown"
BASE COUNT 306 a 243 c 313 g 189 t
ORIGIN

Query Match 49.4%; Score 131.8; DB 6; Length 1051;
Best Local Similarity 82.5%; Pred. No. 2.9e-08;
Matches 151; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 61 AA 120
DB 26 AA 85
OY 121 AAGGGGGGG 180
DB 86 AAGAGAGGC 145
OY 181 GGG 240
DB 146 GAGGGGAGCCGGCGGTGTGTATGTCTTGGCTGGCGCCGCTCAGCCCAAGA 205
OY 241 AAA 243
DB 241 AAA 243

Db 206 AGA 208

RESULT 3
AC025462
LOCUS AC025462
DEFINITION Homo sapiens chromosome 5 clone CTD-2246N22, WORKING DRAFT
SEQUENCE, 18 unordered pieces.
ACCESSION AC025462
AC025462.4 GI:13699662
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 168991)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
2 (bases 1 to 168991)
DOE Joint Genome Institute.
Direct Submission
Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:1711833.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 722347
Center Clone name: CTRB-H1_2246N22

Summary Statistics
Consensus quality: 149454 bases at least Q40
Consensus quality: 156745 bases at least Q20
Consensus quality: 159325 bases at least Q20
Estimated insert size: 168000; pulse field gel estimation
Estimated insert size: 167291; sum-of-ctrls estimation
Quality coverage: 6.53 in Q20 bases; pulse field gel estimation
Quality coverage: 6.56 in Q20 bases; sum-of-ctrls estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1047: contig of 1047 bp in length
* 1048 1147: gap of unknown length
* 1148 2195: contig of 1048 bp in length
* 2196 2295: gap of unknown length
* 2296 3556: contig of 1261 bp in length
* 3557 3656: gap of unknown length
* 3657 4909: contig of 1253 bp in length
* 4910 5009: gap of unknown length
* 5010 6079: contig of 1070 bp in length
* 6080 6179: gap of unknown length
* 6180 8060: contig of 1881 bp in length
* 8160 8160: gap of unknown length
* 8161 11429: contig of 3269 bp in length
* 11430 11529: gap of unknown length
* 11530 13869: contig of 2340 bp in length
* 13870 13969: gap of unknown length
* 13970 16992: contig of 2723 bp in length
* 16993 16992: gap of unknown length
* 16993 19825: contig of 3033 bp in length
* 19826 19926: gap of unknown length
* 19926 26442: contig of 6517 bp in length
* 26443 26542: gap of unknown length
* 26543 37173: contig of 10631 bp in length

	*	37174	37273:	gap of unknown length	
	*	37274	46552:	contig of 9379 bp in .length	
	*	46653	46752:	gap of unknown length	
	*	46753	57449:	contig of 10597 bp in length	
	*	57350	57450:	gap of unknown length	
	*	57450	75018:	contig of 17569 bp in length	
	*	75019	75118:	gap of unknown length	
	*	75119	91122:	contig of 16004 bp in length	
	*	91123	91222:	gap of unknown length	
	*	91223	119455:	contig of 28233 bp in length	
	*	119456	119555:	gap of unknown length	
* * *		119556	168991:	contig of 49436 bp in length.	
FEATURES					
SOURCE			/location/Qualifiers		
			.organism="Homo sapiens"		
			/db_xref="taxon:9606"		
			/chromosome="5"		
			/clone="CTD-2246N22"		
BASE COUNT		46100 a	39450 c	38335 g	43406 t 170.) others
ORIGIN					
Query Match			49.1%;	Score 131; DB 2; Length 168991;	
Best Local Similarity			87.7%; Pred. NO. 3e+08;		
Matches 143;			Conservative 0; Mismatches 20; Indels 0; Gaps 0;		
OY 61	AAA	A	120		
Db 56573	AAA	C	56632		
OY 121	AAA	G	GGGCGGC	180	
Db 56633	AAA	A	ACAGAGGAG	56692	
OY 181	GGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGC	G	223		
Db 56693	GGAGGCCAGCACGACGAGGGGGGAAGAAGCAAGCAAGAG	G	56735		
RESULT 4					
LOCUS AC022129					
DEFINITION Homo sapIiens chromosome 5 clone CTD-2183B13, WORKING DRAFT ;					
SEQUENCE, 40 unordered pieces.					
AC022129					
ACCESSION AC022129..5 GI:13699626					
VERSION HTGS: PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.					
KEYWORDS Homo sapiens.					
SOURCE Homo sapIiens					
ORGANISM Eukaryota; Metazoa; Chordata; Craniota; Vertebrate; Euteleostomi; Mammalia; Euarcharia; Primates; Catarrhini; Homnidae; Homo. DOE Joint Genome Institute. Sequencing of Human Chromosome 5 Unpublished 2 (bases 1 to 214139) DOE Joint Genome Institute. Direct Submission Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:9594660. ----- Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov Project Information Center Project Name: 697863 Center Clone name: CTB-HL_2183B13 ----- Summary Statistics Consensus quality: 177232 bases at least <40 Consensus quality: 190777 bases at least <30					

Consensus quality: 195469 bases at least Q20		
Estimated insert size: 121000; pulse field gel estimation		
Estimated insert size: 210239; sum-of-contrigs estimation		
Quality coverage: 7.99 in Q20 bases; pulse field gel estimation		
Quality coverage: 4.6 in Q20 bases; sum-of-contrigs estimation.		
* NOTE: This is a 'working draft' sequence. It currently		
* consists of 40 contrigs. The true order of the pieces		
* is not known and their order in this sequence record is		
* arbitrary. Gaps between the contrigs are represented as		
* runs of N, but the exact sizes of the gaps are unknown.		
* This record will be updated with the finished sequence		
* as soon as it is available and the accession number will		
* be preserved.		
1	1159:	contrig of 1159 bp in length
*	1160	1259: gap of unknown length
*	1260	2521: contrig of 1262 bp in length
*	2522	2621: gap of unknown length
*	2622	3853: contrig of 1232 bp in length
*	3854	3953: gap of unknown length
*	3954	5111: contrig of 1158 bp in length
*	5112	5211: gap of unknown length
*	5212	6367: contrig of 1156 bp in length
*	6368	6467: gap of unknown length
*	6468	7531: contrig of 1064 bp in length
*	7532	7631: gap of unknown length
*	7632	8836: contrig of 1205 bp in length
*	8837	8936: gap of unknown length
*	8937	10072: contrig of 1136 bp in length
*	10073	10172: gap of unknown length
*	10173	11593: contrig of 1421 bp in length
*	11594	11693: gap of unknown length
*	11694	13594: contrig of 1901 bp in length
*	13595	13694: gap of unknown length
*	13695	15802: contrig of 2108 bp in length
*	15803	15902: gap of unknown length
*	15903	17998: contrig of 2096 bp in length
*	17999	18098: gap of unknown length
*	18099	20026: contrig of 1928 bp in length
*	20027	20126: gap of unknown length
*	20127	22336: contrig of 2210 bp in length
*	22337	22436: gap of unknown length
*	22437	24423: contrig of 1987 bp in length
*	24424	24523: gap of unknown length
*	24524	25992: contrig of 1459 bp in length
*	25993	26092: gap of unknown length
*	26093	28201: contrig of 2109 bp in length
*	28202	28301: gap of unknown length
*	28302	29954: contrig of 1653 bp in length
*	29955	30054: gap of unknown length
*	30055	31259: contrig of 1205 bp in length
*	31260	31359: gap of unknown length
*	31360	33236: contrig of 1877 bp in length
*	33237	33336: gap of unknown length
*	33337	36092: contrig of 2756 bp in length
*	36093	36192: gap of unknown length
*	36193	39292: contrig of 3100 bp in length
*	39293	39392: gap of unknown length
*	39393	41807: contrig of 2415 bp in length
*	41808	41907: gap of unknown length
*	41908	43021: contrig of 1114 bp in length
*	43022	43121: gap of unknown length
*	43122	46643: contrig of 3522 bp in length
*	46644	46743: gap of unknown length
*	46744	49961: contrig of 3218 bp in length
*	49962	50061: gap of unknown length
*	50062	53523: contrig of 3462 bp in length
*	53524	53623: gap of unknown length
*	53624	60457: contrig of 6834 bp in length
*	60458	60557: gap of unknown length
*	60558	64477: contrig of 3920 bp in length
*	64578	64577: gap of unknown length
*	64578	70891: contrig of 6314 bp in length
*	70892	70991: gap of unknown length

	*	70992	72966:	contig of 1975 bp in length
	*	72967	73066:	gap of unknown length
	*	73067	81422:	contig of 8356 bp in length
	*	81423	81522:	gap of unknown length
	*	81523	88228:	contig of 6706 bp in length
	*	88229	88328:	gap of unknown length
	*	91708	91707:	contig of 3379 bp in length
	*	91708	91807:	gap of unknown length
	*	100082	100081:	contig of 8274 bp in length
	*	100182	100181:	gap of unknown length
	*	112696	112695:	contig of 12514 bp in length
	*	112796	112795:	gap of unknown length
	*	124390	124389:	contig of 11594 bp in length
	*	124490	124489:	gap of unknown length
	*	145242	145241:	contig of 20752 bp in length
	*	145342	145341:	gap of unknown length
	*	171395	171394:	contig of 26653 bp in length
	*	171495	171494:	gap of unknown length
	*	171495	214139:	contig of 42645 bp in length.
FEATURES				
source				
				1..214139
				/organism="Homo sapiens"
				/db_xref="taxon:9606"
				/chromosome="5"
				/clone="CTD-2183B18"
				/clone_lib="CalTech human BAC library D"
BASE COUNT	58620 a	46379 c	46197 g	58900 t 4043 others
ORIGIN				
Query Match		48.1%	Score 128.4:	DB 2: Length 214139;
Best Local Similarity	80.2%;	Pred No. 6.3e-08;		
Matches 150;	Conservative	0;	Mismatches 37;	Indels 0; Gaps 0;
OY	31	AAANAAATAAAAAGCACTTATTATTCACAGCAAAAAAAAAAAAAAAAAAAAAAAAAA	90	
Db 171546	AATTAATAATAAAAAATATATATATTAATTAATAAAAAAAAAAAAAAAAAAAAAA	171605		
OY	91	AAA	150	
Db 171606	AA	171665		
OY	151	AAAAAAAAAAAAAAAAAAGCGGGGCGGGGGCGGGGCGGAGCGGGGCGGGGGCGG	210	
Db 171666	AAAAAAAAAAAAAAAAAAGGAGACGACGACGACGACGACGACGACGACGACGACGACG	171725		
OY	211	GCGGGCGG 217		
Db 171726	AGAGGAG 171732			
RESULT 5				
AC083752/c				
LOCUS	AC083752	165563 bp	DNA	linear HTG 30-SEP-2000
DEFINITION	Mus musculus chromosome 5 clone RP23-425D14 strain C57BL6/J,			
ACCSSION	AC083752			
VERSION	AC083752.1 GI:10440604			
KEYWORDS	HTGS_PHASE1; HTGS_DRAFT.			
SOURCE	MUS MUSCULUS.			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
	1 (bases 1 to 165563)			
REFERENCE	Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,			
AUTHORS	Bouffard,G.G., Dietrich,N.L., Gupta,J., Ho,S.-L., Idol,J.,			
	Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B.,			
	Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B.,			
	Stantirlop,S., Thomas,J.W., Thomas,P.J., Tlonsong,E.E.,			
	Touchman,J.W., Tran,J.T., Vogt,J.L., Walker,M.A., Wecherby,K.D. and			
	Green,E.D.			
TITLE	NISC Mouse Sequencing Initiative			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 165563)			

```

AUTHORS      Green, E.D.
TITLE        Direct Submision
JOURNAL      Submitted (30-SEP-2000) NIH Intramural Sequencing Center, 8717
              Grovmont Circle, Galtersburg, MD 20877, USA
COMMENT      -----
              Genome Center
              Center: NIH Intramural Sequencing Center
              Center code: NISC
              Web site: http://www.nisc.nih.gov
              Contact: nisc.mouse@hgtl.nih.gov
              -----
              Project Information
              Center project name: sq
              Center clone name: 425D14
              -----
              Summary Statistics
              Sequencing vector: plasmid; n/a; 100% of reads
              Chemistry: Dye-terminator Big Dye; 100% of reads
              Assembly program: Phrap; version 0.990319
              Consensus quality: 157792 bases at least Q40
              Consensus quality: 160637 bases at least Q30
              Consensus quality: 161879 bases at least Q20
              Insert size: 164000; agarose-fp
              Insert size: 164263; sum-of-contigs
              Quality coverage: 4.42x in Q20 bases; agarose-fp
              Quality coverage: 4.41x in Q20 bases; sum-of-contigs
              -----
              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 14 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              -----
              1      3216: contig of 3216 bp in length
              *      3217      3316: gap of unknown length
              *      3317      7069: contig of 3753 bp in length
              *      7070      7169: gap of unknown length
              *      7170      10025: contig of 2856 bp in length
              *      10026      10125: gap of unknown length
              *      10126      13978: contig of 3853 bp in length
              *      13979      14078: gap of unknown length
              *      14079      18906: contig of 4828 bp in length
              *      18907      19006: gap of unknown length
              *      19007      28064: contig of 9058 bp in length
              *      28065      28164: gap of unknown length
              *      28165      37349: contig of 9185 bp in length
              *      37350      37449: gap of unknown length
              *      37450      43305: contig of 5856 bp in length
              *      43306      43405: gap of unknown length
              *      43406      55430: contig of 12025 bp in length
              *      55431      55530: gap of unknown length
              *      55531      70448: contig of 14918 bp in length
              *      70449      70548: gap of unknown length
              *      70549      87145: contig of 16597 bp in length;
              *      87146      87245: gap of unknown length
              *      87246      104503: contig of 17258 bp in length
              *      104504      104603: gap of unknown length
              *      135036      135036: contig of 30433 bp in length
              *      135037      135136: gap of unknown length
              *      135137      165563: contig of 30427 bp in length.
              -----
              Location/Qualifiers
              1.165563
              /organism="Mus musculus"
              /strain="C57BL6/J"
              /db_xref="taxon:10090"
              /chromosome="5"
              /clone="RP23-425D14"
              /clone_lib="RPCT mouse BAC library 23"
              1.3216
              /note="assembly_fragment"
              3317.7069
              /note="assembly_fragment"
              7170.10025
              /note="assembly_fragment"

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Query Match	47.9%;	Score 128;	DB 2;	Length 165563;
Best Local Similarity	82.7%;	Pred. No. 7.1e-08;		
Matches 143; Conservative	0;	Mismatches 30;	Indels 0;	Gaps 0;

RESULT	6
HSMB05518	
LOCUS	HSMB05518
DEFINITION	Homo sapiens mRNA; CDNA DKFZp62P135 (from clone DKFZp62P135).
ACCESSION	AL834428
VERSION	AL834428.1 GI:21740150

ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT
Homo sapiens Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.	1 (bases 1 to 2319) Bloecher, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and Wiemann, S.	Direct Submission Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GfR (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
		This clone (DKFZ762F135) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/ .

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1. .2319 Location/Qualifiers
FEATURES
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        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /map="16p13.3"
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Query Match	47.28;	Score 126;	DB 9;	Length 2319;
Best Local Similarity	89.48;	Pred. No. 1.5e-07;		
Matches 135; Conservative	0;	Mismatches 16;	Indels 0;	Gaps 0;

RESULT 7	
BC018613	
LOCUS	BC018613 3307 bp mRNA linear ROD 07-AUG-2002
DEFINITION	Mus musculus, secretory carrier membrane protein 5, clone MGC:27646
IMAGE	4511417, mRNA, complete cds.
ACCESSION	BC018613
VERSION	BC018613..1 GI:17391342
KEYWORDS	MGC.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK	COMMENT
1	(bases 1 to 3307)	Strausberg, R. Direct Submission Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: The Cepko Laboratory CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	

SOURCE ORGANISM

Norway rat.
Eutatus norvegicus
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata: Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE AUTHORS

1 (bases 1 to 162610)
Mizny,D.M., Adams,C., Adlo-Oduola,B., Ali-Usman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralungu,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieve,M., Brown,M., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,U., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Deckerich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsl,F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Lounseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Mareshwar,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,R., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nuygen,N., Nickerson,E., Nwokenkwo,S., Ogul,M., Okunnu,G.,
Oragunye,N., Oyiedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoshitari,H., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svaltek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,J., Vera,Y., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczek,R., Woodden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

TITLE

Unpublished

JOURNAL

2 (bases 1 to 162610)

REFERENCE

Worley,K.C.

AUTHORS

Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

JOURNAL

3 (bases 1 to 162610)

REFERENCE

Worley,K.C.

AUTHORS

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

JOURNAL

On Jul 11, 2002 this sequence version replaced gl:18700977.

COMMENT

Center: Baylor College of Medicine
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GLJF
Center clone name: CH230-52B4
Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 97112 bases at least Q40
Consensus quality: 101400 bases at least Q30
Consensus quality: 104193 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 74 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1058: contig of 1058 bp in length
1059 1158: gap of unknown length
1159 2791: contig of 1633 bp in length
2791 2891: gap of unknown length
2891 4019: contig of 1128 bp in length
4019 4119: gap of unknown length
4119 5571: contig of 1452 bp in length
5571 5671: gap of unknown length
5671 6685: contig of 1014 bp in length
6685 6785: gap of unknown length
6785 8048: contig of 1263 bp in length
8048 8149: gap of unknown length
8149 9259: contig of 1111 bp in length
9259 9359: gap of unknown length
9359 10466: contig of 1107 bp in length
10466 10566: gap of unknown length
10566 11706: contig of 1140 bp in length
11706 11806: gap of unknown length
11806 13242: contig of 1436 bp in length
13242 13342: gap of unknown length
13342 14844: contig of 1502 bp in length
14844 14944: gap of unknown length
14944 16544: contig of 1510 bp in length
16544 16554: gap of unknown length
16554 17738: contig of 1184 bp in length
17738 17838: gap of unknown length
17838 19023: contig of 1185 bp in length
19023 19123: gap of unknown length
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20397 20497: gap of unknown length
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23141 24986: contig of 1845 bp in length
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28168 28268: gap of unknown length
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29834 29934: gap of unknown length
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31255 31356: gap of unknown length
31356 32958: contig of 1603 bp in length
32958 34601: contig of 1543 bp in length
34601 34701: gap of unknown length
34701 36212: contig of 1511 bp in length
36212 36312: gap of unknown length
36312 37363: contig of 1051 bp in length
37363 37463: gap of unknown length
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38982 39082: gap of unknown length
39082 40692: contig of 1510 bp in length
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Query Match 46.7% Score 124.8; DB 2; Length 162610;
Best Local Similarity 68.8%; Pred. No. 1.0e-07;
Matches 139; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 22 AGAGCCCTGAAATATAAACAACCTATTATTCAGTGAATAAAAAAAAAAAAAAAAAA 81
Db 112921 ANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 112980

QY 82 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 141
Db 112981 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 113040

QY 142 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGG 201
Db 113041 AAAAAAAAAAAAAAAAAAGAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 113100

QY 202 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 223
Db 113101 AGGGGGAGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 113122

RESULT 10
BC025755 1661 bp mRNA linear PRI 11-MAR-2002
LOCUS BC025755
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DEFINITION Homo sapiens, similar to RIKEN cDNA 3110080J08 gene, clone
ACCESSION MGC:35561 IMAGE:5202281, mRNA, complete cds.
VERSION BC025755.1 GI:19343632
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1661)
AUTHORS Strausberg, R.
JOURNAL Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastaglio, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov
Series: IRAC Plate: 49 Row: d Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES
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location/Qualifiers
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/organism="Homo sapiens"
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/protein_id="AA25755.1"
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/translation="MOSNRHYVITLIDSSRRPAGKATIGFVGYKKLPVLDYRAH
NEVEPLCIDFYTHESVORHGRRELFOYMLQEREVHQALDRSQKLFKLNHYH
LEETVPOVNNFVIFEGFPAHQHRRPPAPSRATRHRSRAAVDPTPAAPARKLPKRRE
GDIKPYSSSREMGLOPVW"
BASE COUNT 544 a 453 c 312 g 352 t
ORIGIN
Query Match 46.7% Score 124.6; DB 9; Length 1661;
Best Local Similarity 87.2%; Pred. No. 2.3e-07;
Matches 136; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 16 GTCTCTAGAGCCCTGAAATATAAACAACCTATTATTCAGTGAATAAAAAAAAAA 75
Db 1470 GTATCTTTAAACGAGACCAATATAAGTATTATTTATTCACAAAAA 1529

QY 76 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 135
Db 1530 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1589
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OY 136 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 171
|||||
DB 1590 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1625

RESULT 11
AC087147
LOCUS AC087147
DEFINITION Mus musculus clone RP23-303117, WORKING DRAFT SEQUENCE, 12
unordered pieces.
AC087147
VERSION AC087147.1 GI:11610873
HTG: HTGS_PHASE1, HTGS_DRAFT.
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE DOE Joint Genome Institute.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 133276)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1853433
Center Clone name: RPCI-23_303117

Summary Statistics
Consensus quality: 123774 bases at least Q40
Consensus quality: 125756 bases at least Q10
Consensus quality: 127025 bases at least Q20
Estimated insert size: 160790; agarose-gel estimation
Estimated insert size: 132176; sum-of-contigs estimation
Quality coverage: 9.26 in Q20 bases; agarose-gel estimation
Quality coverage: 11.26 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1651: contig of 1651 bp in length
* 1652 1751: gap of unknown length
* 1752 3085: contig of 1334 bp in length
* 3086 3186: gap of unknown length
* 3186 6343: contig of 3158 bp in length
* 6344 6443: gap of unknown length
* 6444 10463: contig of 4019 bp in length
* 10463 10563: gap of unknown length
* 10563 14968: contig of 4406 bp in length
* 14968 15068: gap of unknown length
* 15068 18263: contig of 3195 bp in length
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* 18264 22627: contig of 4264 bp in length
* 22627 22728: gap of unknown length
* 22728 36171: contig of 13444 bp in length
* 36171 36272: gap of unknown length
* 36272 46624: contig of 10353 bp in length
* 46624 46724: gap of unknown length
* 46724 67169: contig of 20445 bp in length
* 67169 67270 94369: contig of 27100 bp in length
* 67270

* 94370 94469: gap of unknown length
* 94470 133276: contig of 38807 bp in length.
FEATURES
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/db_xref="taxon:10090"
/clone="RP23-303117"
/clone_lib="RPCI mouse BAC library 23"
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ORIGIN
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Best Local Similarity 77.0%; Pred. No. 1.9e-07;
Matches 151; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
OY 31 AANAATATAACACTTATTTATCCAGTGAAAAA 90
|||
DB 46145 AAAAAAAAAAAAAAAAAACAAACAAAAA 46204
OY 91 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 150
|||
DB 46205 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 46264
OY 151 AAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGA 210
|||
DB 46265 AAAAAAAAAACAAAAAAGCAGAAAGCAAGCA 46324
OY 211 GGGGGGGGGGGGGGGGGG 226
DB 46325 AGAGGAAGGGGAAACG 46340
RESULT 12
HSM804650
LOCUS HSM804650
DEFINITION Homo sapiens mRNA: cDNA DKFP686C0734 (from clone DKFP686C0734).
ACCESSION AL833337
VERSION AL833337.1 GI:21733972
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2975)
Otenwelder, B., Oberwarter, B., Mewes, H.W., Well, B., Amid, C. and
Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuberger, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFP686C0734) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.
FEATURES
source
1. 2975
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFP686C0734"
/issue_type="cDNA-collection"
/clone_lib="686 (synonym: hlc3). Vector pSPORT1-Sfi; host
DH10B; sites SfiI + SfiIB"
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BASE COUNT 2812 . 2817
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BASE COUNT 1295 a 460 c 518 g 702 t
ORIGIN
Query Match 46.6%; Score 124.4; DB 9; Length 2975;
Best Local Similarity 83.8%; Pred. No. 2.4e-07;

[illegible]

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* 61741 63763: contig of 2023 bp in length
* 63764 63863: gap of unknown length
* 63864 65024: contig of 1161 bp in length
* 65025 65124: gap of unknown length
* 65125 66664: contig of 1540 bp in length
* 66665 66764: gap of unknown length
* 66765 69128: contig of 2364 bp in length
* 69129 69228: gap of unknown length
* 69229 70931: contig of 1703 bp in length
* 70932 71031: gap of unknown length
* 71032 72459: contig of 1428 bp in length
* 72460 72559: gap of unknown length
* 72560 74798: contig of 2239 bp in length
* 74799 74898: gap of unknown length
* 74899 77383: contig of 2485 bp in length
* 77384 77483: gap of unknown length
* 77484 79590: contig of 2107 bp in length
* 79591 79690: gap of unknown length
* 79691 80939: contig of 1249 bp in length

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Query Match 46.2%; Score 123.4; DB 2; Length 169404;
 Best Local Similarity 75.1%; Pred. No. 2.7e-07;
 Matches 145; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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QY 31 AANATATAAAACACTATTTCACAGTGAATAAAAAAAAAAAAAAAAAAAAAA 90
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79206 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG 79265

QY 91 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 150
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79266 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 79325

QY 151 AAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGGAGGGGGGGGGGGGGG 210
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79326 AAAAAAAAAAAAAAAAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 79385

QY 211 GGGGGGGGGGGG 223
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79386 AGGAGAGAGAGG 79398

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Search completed: March 21, 2003, 15:55:37
 Job time : 2416.44 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 11:28:30 ; Search time 193.227 Seconds
(without alignments)
3111.799 Million cell updates/sec

Title: US-09-823-101-9

Perfect score: 267

Sequence: 1 actcactgctcagctc.....aagagagaaannccttgat 267

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263	98.5	267	22	AAH43643 SSG #9. Homo sapi
2	148.4	55.6	382	22	AAI87526 Human polynucleoti
3	134.6	50.4	408	22	AAI83619 Human polynucleoti
4	134.2	50.3	452	22	AAI83052 Human polynucleoti
5	132.6	49.7	425	22	AAI92106 Human polynucleoti
6	132.4	49.6	448	22	AAI80552 Human polynucleoti
7	131.8	49.4	1051	21	AAZ91918 Murine mahogany pr
8	130.8	49.0	506	22	AAI83507 Human polynucleoti
9	130.8	49.0	903	22	AAI87708 Human polynucleoti

10	130.4	48.8	401	22	AAI85430 Human polynucleoti
11	127.2	47.6	366	22	AAI83312 Human polynucleoti
12	127.2	47.6	416	22	AAI89032 Human polynucleoti
13	127.2	47.6	451	23	ABV56778 Human prostate exp
14	126.6	47.4	398	22	AAI88388 Human polynucleoti
15	126.6	47.4	414	22	AAI84786 Human polynucleoti
16	125.6	47.0	481	23	ABV56248 Human prostate exp
17	125.4	47.0	389	22	AAI88514 Human polynucleoti
18	125	46.8	160	22	AAE24360 Retroviral recomb
19	125	46.8	178	22	AAE24361 Retroviral recomb
20	125	46.8	208	22	AAE24363 Retroviral recomb
21	125	46.8	472	23	ABV49907 Human prostate exp
22	124.8	46.7	391	23	ABV08149 Human prostate exp
23	124.8	46.7	394	22	AAI83453 Human polynucleoti
24	124.6	46.7	430	22	AAI85300 Human polynucleoti
25	124.6	46.7	698	22	AAI86559 Human novel protei
26	124.6	46.7	698	22	AAI88206 cDNA encoding for
27	124.6	46.7	698	22	AAI88206 Human digestive sy
28	124.2	46.5	2674	24	ABA94500 Human proto-oncoge
29	124	46.4	412	22	AAI87374 Human polynucleoti
30	124	46.4	1204	22	AAI63823 Human polynucleoti
31	123.6	46.3	396	23	ABV57596 Human prostate exp
32	123.6	46.3	427	22	AAI83024 Human polynucleoti
33	123.4	46.2	317	23	ABV58763 Human prostate exp
34	123.4	46.2	452	23	ABV59282 Human prostate exp
35	123.2	46.1	528	23	ABV58464 Human prostate exp
36	122.8	46.0	464	23	ABV55314 Human prostate exp
37	122.4	45.8	411	22	AAI85431 Human polynucleoti
38	122.4	45.8	490	23	ABV57059 Human prostate exp
39	122.4	45.8	12007	24	ABL32717 Human immune syste
40	122.2	45.8	488	23	ABV58909 Human prostate exp
41	122.2	45.8	502	23	ABV58733 Human prostate exp
42	122.2	45.8	1503	22	AAK58876 Human immune/haema
43	122.2	45.8	7765	22	AAI26497 Human breast cance
44	122	45.7	375	23	ABV44911 Human prostate exp
45	122	45.7	380	23	ABV58659 Human prostate exp

ALIGNMENTS

RESULT 1	
AAH43643	
AAH43643 standard; cDNA; 267 BP.	
AC	AAH43643;
AC	
DT	21-JAN-2002 (first entry)
AC	
DE	SSG #9.
XX	
KW	Stomach cancer specific gene; SSG; polymerase chain reaction; PCR;
KW	amplify; primer; subtracted library; expressed sequence tag; EST; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200175169-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001MO-US10591.
XX	
PR	30-MAR-2000; 2000US-193095P.
XX	
XX	(DIAD-) DIADEXUS INC.
PA	
XX	Pluta J, Chen S, Hu P, Recipon H, Macina RA;
PI	
XX	WPI; 2001-656992/75.
DR	
XX	New Stomach Cancer Specific Genes, useful for diagnosing, monitoring,
PT	staging, imaging or treating cancer, particularly stomach cancer
XX	

PS Claim 1: Page 68; 71pp; English.

XX The sequences given in AHA4636-47 represent Stomach Cancer Specific

CC Genes (SSC's). These polynucleotides were isolated using a PCR based

CC subtractive hybridisation method on subtracted libraries which were

CC generated for stomach. The cDNA libraries contained expressed sequence

CC tags (EST's) from genes that are stomach cancer specific or are

CC upregulated in stomach. These polynucleotides and the corresponding

CC encoded polypeptides are useful for diagnosing, monitoring, staging,

CC imaging or treating cancer, particularly stomach cancer.

CC

XX

SQ Sequence 267 BP; 147 A; 33 C; 62 G; 21 T; 4 other;

Query Match 98.5%; Score 263; DB 22; Length 267;

Best Local Similarity 100.0%; Pred. No. 2.9e-21;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACTTACCGTCTCAGTCTGAGCCCTGAGANATTAACAACTATTATTCACATG 60

DB 1 ACTTACCGTCTCAGTCTGAGCCCTGAGANATTAACAACTATTATTCACATG 60

OY 61 AA 120

DB 61 AA 120

OY 121 AAGGGGGG 180

DB 121 AAGGGGGG 180

OY 181 GGG 240

DB 181 GGG 240

OY 241 AAACAAAAAGAGAGAAAAAANCNTTGAT 267

DB 241 AAACAAAAAGAGAGAAAAAANCNTTGAT 267

RESULT 2

AAI87526

ID AAI87526 standard; cDNA: 382 BP.

XX AAI87526;

DT 06-NOV-2001 (first entry)

XX Human polynucleotide SEQ ID NO 7586.

DE

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukemia;

KW nervous system disorders; arthritis; inflammation; ss.

XX Homo sapiens.

OS

XX WO200164835-A2.

PN

XX 07-SEP-2001.

PD

XX 26-FEB-2001; 2001WO-US04927.

PF

XX 28-FEB-2000; 2000US-0515126.

PR

XX 18-MAY-2000; 2000US-0577409.

PR

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Liu C, Drmanac RT;

PI

XX WPI; 2001-514838/56.

DR

XX P-PSDB; AA007595.

DR

XX Isolated nucleic acids and polypeptides, useful for preventing

PT diagnosing and treating e.g. leukemia, inflammation and immune

PT

PT disorders -

XX

XX Claim 1: SEQ ID NO 7586; 1399pp + Sequence Listing; English.

XX

CC The invention relates to human polynucleotides (AAI79941-AAI93841) and

CC the encoded proteins (AAO0010-AAO13910) that exhibit actively elating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, hematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukemia, nervous system disorders, arthritis and

CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pcl_sequences.

XX

SQ Sequence 382 BP; 265 A; 18 C; 69 G; 17 T; 13 other;

Query Match 55.6%; Score 148.4; DB 22; Length 382;

Best Local Similarity 86.6%; Pred. No. 8.8e-09;

Matches 161; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 31 AANAATAAACAACCTATTATTCAGTGAATAAAAAAAAAAAAAAAAAAAAAA 90

DB 93 AA 152

OY 91 AA 150

DB 91 AA 150

OY 153 AA 212

DB 153 AA 212

OY 151 AAAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 210

DB 151 AAAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 210

OY 211 GGGGGG 216

DB 211 GGGGGG 216

OY 273 GGAGGG 278

DB 273 GGAGGG 278

RESULT 3

AAI83619

ID AAI83619 standard; cDNA: 408 BP.

XX AAI83619;

DT 06-NOV-2001 (first entry)

XX Human polynucleotide SEQ ID NO 3679.

DE

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukemia;

KW nervous system disorders; arthritis; inflammation; ss.

XX Homo sapiens.

OS

XX WO200164835-A2.

PN

XX 07-SEP-2001.

PD

XX 26-FEB-2001; 2001WO-US04927.

PF

XX 28-FEB-2000; 2000US-0515126.

PR

XX 18-MAY-2000; 2000US-0577409.

PR

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Liu C, Drmanac RT;

PI

XX WPI; 2001-514838/56.

DR

XX

DR

```

DR P-PSDB;AA003688.
xx
xx Isolated nucleic acids and polypeptides, useful for preventing
xx diagnosing and treating e.g. leukaemia, inflammation and immune
xx disorders -
xx
xx Claim 1; SEQ ID NO 3679; 1399pp + Sequence Listing; English.
xx
xx The invention relates to human polynucleotides (AA179941-AA193841) and
xx the encoded proteins (AA000010-AA013910) that exhibit activity elating to
xx cytokine, cell proliferation or cell differentiation on which may induce
xx production of other cytokines in other cell populations. The
xx polypeptides and polypeptides are useful in gene therapy, vaccines or
xx peptide therapy. The polypeptides have various cytokine-like activities,
xx e.g. stem cell growth factor activity, haematopoiesis regulating
xx activity, tissue growth factor activity, immunomodulatory activity and
xx activin/inhibin activity and may be useful in the diagnosis and/or
xx treatment of cancer, leukaemia, nervous system disorders, arthritis and
xx inflammation.
xx Note: The sequence data for this patent did not form part of the printed
xx specification, but was obtained in electronic format directly from WIPO
xx at ftp.wipo.int/pub/published_pct_sequences.
xx
xx Sequence 408 BP; 201 A; 33 C; 57 G; 103 T; 14 other;
xx
xx Query Match 50.4%; Score 134.6; DB 22; Length 408;
xx Best Local Similarity 81.6%; Pred. No. 2.8e-07;
xx Matches 146; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
xx
xx 36 TAAAAACACACTTATTTTATCCAGTGAIAAAAAAAAAAAAAAAAAAAAAA 95
xx ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx 207 TAAATATATATATCTTATATACCAAAAAAAAAAAAAAAAAAAAAA 266
xx ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx Oy AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 155
xx ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx Db AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 326
xx ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx Oy 156 AAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 214
xx ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx Db 327 AAAAAAAAAAAAAANNNNNNNNNGGGGGGGGGGNAAAAAAAAAANNNGGGGGGGGGGG 385
xx ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx
xx RESULT 4
xx AAI83052
xx ID AAI83052 standard; cDNA; 452 BP.
xx AC
xx AA183052;
xx
xx DT 06-NOV-2001 (first entry)
xx
xx DE Human polynucleotide SEQ ID NO 3112.
xx
xx KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
xx vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
xx tissue growth factor; immunomodulatory; cancer; leukaemia;
xx nervous system disorders; arthritis; inflammation; ss.
xx
xx OS Homo sapiens.
xx
xx PN WO200164835-A2.
xx
xx PD 07-SEP-2001.
xx
xx PE 26-FEB-2001; 2001WO-US04927.
xx
xx PR 28-FEB-2000; 2000US-0515126.
xx
xx PR 18-MAY-2000; 2000US-0577409.
xx
xx PA (HYSE-) HYSEQ INC.
xx
xx Tang YT, Liu C, Drmanac RT;
xx
xx WPI: 2001-514838/56.
xx

```

DR	P-PSDB: AAO03121.	
XX	Isolated nucleic acids and polypeptides, useful for preventing	
PT	diagnosing and treating e.g. leukaemia, inflammation and immune	
PT	disorders -	
XX		
PS	Claim 1; SEQ ID NO 3112: 1399pp + Sequence Listing; English.	
XX		
CC	The invention relates to human polynucleotides (AA179941-AA193841) and	
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to	
CC	cyclokin, cell proliferation or cell differentiation or which may induce	
CC	production of other cytokines in other cell populations. The	
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or	
CC	peptide therapy. The polypeptides have various cytokine-like activities,	
CC	e.g. stem cell growth factor activity, haematopoiesis regulating	
CC	activity, tissue growth factor activity, immunomodulatory activity and	
CC	activin/inhibin activity and may be useful in the diagnosis and/or	
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and	
CC	inflammation.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
SQ	Sequence 452 BP; 227 A; 52 C; 99 G; 67 T; 7 other;	
	Query Match 50.3%; Score 134.2; DB 22; Length 452;	
	Best Local Similarity 93.3%; Pred. NO. 3e-07;	
	Matches 139; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
QY	61 AA 120	
DB	127 AA 186	
QY	121 AA 180	
DB	187 AA 246	
QY	181 GGGGGGGGGGGGGGGGGGGGGGGGGGGGG 209	
DB	247 GGGGGGAAAAAAAAAAGGGGGGGGGGGGG 275	
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ID	AA192106	
ID	AA192106 standard; cDNA: 425 BP.	
XX	AA192106;	
AC		
DT	06-NOV-2001 (first entry)	
XX		
DE	Human polynucleotide SEQ ID NO 12166.	
XX		
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;	
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;	
KW	nervous system disorders; arthritis; inflammation; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200164835-A2.	
XX		
PD	07-SEP-2001.	
XX		
PF	26-FEB-2001; 2001WO-US04927.	
XX		
PR	28-FEB-2000; 2000US-0515126.	
PR	18-MAY-2000; 2000US-0577409.	
XX		
RA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Drmanac RT;	
XX		
DR	WPI: 2001-514838/56.	

DR P-PSDB: AA012175.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 1: SEQ ID NO 12166; 1399pp + Sequence Listing: English.
 XX
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 425 BP; 188 A; 37 C; 118 G; 82 T; 0 other:
 Query Match 49.7%; Score 132.6; DB 22; Length 425;
 Best Local Similarity 88.3%; Pred. No. 4.6e-07;
 Matches 144; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 OY 61 AA 120
 DB 77 AA 136
 OY 121 AAGGCGCGG 180
 DB 137 AAGGCGCGG 196
 OY 181 GGGGGGGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGG 223
 DB 197 GGGGTTTAAATGCGAAGCGGGGGGGGGGGGGGGGGG 239
 RESULT 6
 AA180552
 ID AA180552 standard: cDNA; 448 BP.
 XX
 AC AA180552;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 612.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PF 26-FEB-2001; 2001WO-US04927.
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSEQ-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT;
 DR WPI; 2001-514838/56.

DR P-PSDB: AA000621.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 1: SEQ ID NO 612; 1399pp + Sequence Listing: English.
 XX
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 448 BP; 214 A; 31 C; 146 G; 52 T; 5 other:
 Query Match 49.6%; Score 132.4; DB 22; Length 448;
 Best Local Similarity 76.2%; Pred. No. 4.7e-07;
 Matches 163; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
 OY 41 ACAAATTAATTTATCCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 100
 DB 36 ACTAGTTATATCTATTAATTAACAAATTTCTACTAAAAAAAAAAAAAAAAA 95
 OY 101 AA 160
 DB 96 AA 155
 OY 161 AAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 220
 DB 156 AAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 215
 OY 221 GGGCCGCCCCGCCCCCAAAACAAAGAGAG 254
 DB 216 GGGAGGGGGAAGAAAGACACAAAGAGGGG 249
 RESULT 7
 AA291918
 ID AA291918 standard: cDNA; 1051 BP.
 XX
 AC AA291918;
 XX
 DT 08-JUN-2000 (first entry)
 XX
 DE Murine mahogany protein coding sequence akml1004.
 XX
 KW Mahogany gene; mouse; mg gene; regulatory defect; gene therapy; obesity;
 KW weight regulation; cell therapy; body weight disorder; cachexia;
 KW anorexia; hyperpigmentation; increased metabolic rate disorder;
 KW hyperphagia; Antioesity; antianorexic; anticachexic; ss.
 XX
 OS Mus sp.
 XX
 PN WO200005373-A2.
 PD 03-FEB-2000.
 PF 21-JUL-1999; 99WO-US16484.
 PR 21-JUL-1998; 98US-0093630.
 PR 20-OCT-1998; 98US-0104978.
 PR 05-FEB-1999; 99US-0245041.
 XX

PA (MILL-) MILLENIUM PHARM INC.
XX
XX Moore K, Nagle DL;
XX
XX WPI: 2000-195103/17.
DR P-PSDB: AAY81805.
XX
XX New human and murine mahogany genes, useful, e.g. for diagnosis and
PT treatment of body weight disorders -
XX
XX
PS Claim 1: Fig 9a: 188pp: English.
XX
XX This sequence represents a murine mahogany gene of the invention.
CC The mahogany genes are used: (i) to produce recombinant mahogany (mg)
CC proteins (II); (ii) as a source of antisense, ribozyme or triplex-forming
CC therapeutics; (iii) as a source of diagnostic probes and primers for
CC detecting expression of mg genes or mutations, regulatory defects, in
CC this gene, or for isolation of related sequences; and
CC (iv) in (cell-based) gene therapy. (ii) are used to raise specific
CC antibodies (Ab); to identify other (extra)cellular products involved in
CC weight regulation, and to screen for agents that disrupt interaction
CC between (ii) and other macromolecules. The Ab are used to detect abnormal
CC levels (or function) of (ii) (for diagnosis, prognosis or monitoring of
CC treatment); to evaluate (ii)-expressing cells intended for cell therapy,
CC and as therapeutic mg inhibitors. Cells that express the mg gene (or
CC contain the mg polypeptide) are used to identify agents (A) that modulate
CC mg activity. (A) are potentially useful for the treatment of body weight
CC disorders, particularly obesity, cachexia or anorexia, or other
CC conditions associated with the mg gene such as hyperpigmentation,
CC hyperphagia and disorders that result in increased metabolic rate.
XX
XX Sequence 1051 BP; 306 A; 243 C; 313 G; 189 T; 0 other:

Query Match 49.4%; Score 131.8; DB 21; Length 1051;
Best Local Similarity 82.5%; Pred. No. 4.6e-07;
Matches 151; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 61 AA 120
DB 26 AA 85
QY 121 AA 180
DB 86 AA 145
QY 181 GGG 240
DB 146 GAAAGGGAGCGCGGTGCTGTATGTGCTGCTGCGGCAGCCAGCA 205
QY 241 AAA 243
DB 206 ACA 208
RESULT 8
AA183507
ID AA183507 standard; cDNA: 506 BP.
XX
XX AA183507;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 3567.
XX
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX

PD 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Dirmannac RT;
PI WPI: 2001-514838/56.
DR P-PSDB: AAO03576.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. Leukaemia, inflammation and immune
PT disorders -
XX
XX
PS Claim 1: SEQ ID NO 3567; 1399pp + Sequence Listing: English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 506 BP; 234 A; 50 C; 111 G; 106 T; 5 other:

Query Match 49.0%; Score 130.8; DB 22; Length 506;
Best Local Similarity 82.0%; Pred. No. 6.9e-07;
Matches 150; Conservative 0; Mismatches 33; Indels 1; Gaps 0;

QY 29 TGAANAATATAAACAATATTATTCAGTGAATAAAAAAAAAAAAAAAAAAAAAA 88
DB 133 TTAATATAGCAATATTTGAATAATTAAGAAACAAAGTTAAAAAAAAAAAAAAA 192
QY 89 AA 148
DB 193 AA 252
QY 149 AA 208
DB 253 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGGGTTTAAATGTGACAGAGGGG 312
QY 209 GCG 211
DB 313 GCG 315
RESULT 9
AA187708
ID AA187708 standard; cDNA: 903 BP.
XX
XX AA187708;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 7768.
XX
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
XX

```
OS Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSEQ-) HYSEQ INC.
XX
XX Tang YF, Liu C, Dimañac RT;
XX
XX WPI: 2001-514838/56.
XX
XX P-PSDB: AAO07777.
XX
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukemia, inflammation and immune
XX disorders -
XX
XX Claim 1; SEQ ID NO 7768; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 903 BP; 297 A; 208 C; 192 G; 199 T; 7 other:
XX
XX Query Match 49.0%; Score 130.8; DB 22; Length 903;
XX Best Local Similarity 84.2%; Pred. No. 6.1e-07;
XX Matches 144; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
XX
XX QY 31 AANAATAAACAACTTTTATCCAGTGAATAAAAAAAAAAAAAAAAAAAAAA 90
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 231 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 290
XX
XX QY 91 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 150
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 291 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 350
XX
XX QY 151 AAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGGG 201
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 351 AAAAAAAAAAAAAAAAANNNNNGGGGGGGGGGAGGAGGGGGG 401
XX
XX
XX RESULT 10
XX AA185430
XX ID AA185430 standard; CDNA: 401 BP.
XX
XX AC AA185430;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human polynucleotide SEQ ID NO 5490.
XX
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukemia;
XX KW nervous system disorders; arthritis; inflammation; ss.
XX
```

```
OS Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSEQ-) HYSEQ INC.
XX
XX Tang YF, Liu C, Dimañac RT;
XX
XX WPI: 2001-514838/56.
XX
XX P-PSDB: AAO05499.
XX
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukemia, inflammation and immune
XX disorders -
XX
XX Claim 1; SEQ ID NO 5490; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 401 BP; 181 A; 75 C; 71 G; 67 T; 7 other:
XX
XX Query Match 48.8%; Score 130.4; DB 22; Length 401;
XX Best Local Similarity 85.9%; Pred. No. 8e-07;
XX Matches 140; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
XX
XX QY 61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 196 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 255
XX
XX QY 121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 180
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 256 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 315
XX
XX QY 181 GGGGGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGG 223
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 316 GGGGGGGGGGAGAGGAGGAGGGGGGGGGGGGGG 358
XX
XX
XX RESULT 11
XX AA183212
XX ID AA183212 standard; CDNA: 366 BP.
XX
XX AC AA183212;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human polynucleotide SEQ ID NO 3272.
XX
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukemia;
XX KW nervous system disorders; arthritis; inflammation; ss.
XX
```


XX pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX WO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US05171.
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
PI WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX Claim 1; Page 10942; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 451 BP; 210 A; 76 C; 104 G; 61 T; 0 other;
SQ
Query Match 47.6%; Score 127.2; DB 23; Length 451;
Best Local Similarity 74.6%; Pred. No. 1.7e-06;
Matches 159; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
OY 22 AGAGCCCTGAANAATTAACACTTATTTATCCAGTGAAAGAAAAA 81
DB 124 AGTGACTAGACATCTAATAAAGCTCTTCACAAAAA 183
OY 82 AA 141
DB 184 AA 243
OY 142 AAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGAGGGGGG 201
DB 244 AAAAAAAAAAAATTTTAAAAAAGGGGGGGGGGGGGGGGGGGGGGG 303
OY 202 GGG 234
DB 304 TCCCCCTTAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 336

XX 06-NOV-2001 (first entry)
PT Human polynucleotide seq ID NO 8448.
DE Human polynucleotide seq ID NO 8448.
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX Homo sapiens.
OS WO200164835-A2.
XX 07-SEP-2001.
XX 26-FEB-2001; 2001WO-US04927.
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-514838/56.
DR P-PSDB; AA008457.
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX Claim 1; SEQ ID NO 8448; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI9941-AAI93841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX Sequence 398 BP; 271 A; 20 C; 64 G; 43 T; 0 other;
SQ
Query Match 47.4%; Score 126.6; DB 22; Length 398;
Best Local Similarity 82.8%; Pred. No. 2.1e-06;
Matches 144; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
OY 31 AANAATTAACCACTTATTTATCCAGTGAAAGAAAAA 90
DB 145 AA 204
OY 91 AA 150
DB 205 AA 264
OY 151 AAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 204
DB 265 AAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 318


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XX 06-NOV-2001 (first entry)
DT
XX
DE Human polynucleotide SEQ ID NO 4846.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PE 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
XX
P-PSDB: AAO04855.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 1; SEQ ID NO 4846; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 414 BP; 174 A; 51 C; 96 G; 93 T; 0 other;

Query Match          47.4%; Score 126.6; DB 22; Length 414;
Best Local Similarity 90.6%; Pred. No. 2.1e-06;
Matches 135; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120
   |||
D9 69 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 128
   |||
QY 121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGG 180
   |||
DB 129 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGGG 188
   |||
QY 181 GGGGGGGGGGGGAGGGGGGGGGGGGGGGG 209
   |||
DB 189 GGGTTTTTTAAATAATGGGGGGGGGG 217
   |||

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Search completed: March 21, 2003, 11:54:16
 Job time : 201.427 secs

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: APPLICANT: GAN, Weiniu et al.
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: FILE REFERENCE: THEREOF
: CURRENT APPLICATION NUMBER: US/09/817,180
: CURRENT FILING DATE: 2001-03-27
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 1
: LENGTH: 2674
: TYPE: DNA
: ORGANISM: Human
: US-09-817-180-1

Query Match
Best Local Similarity 46.5%; Score 124.2; DB 4; Length 2674;
Matches 141; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 2 CTTACCTGCTCAGTCCTAGAGCCCTGANAATTAACCACTTATTATTCAGTGA 61
Db 2488 CTGCTGCTGCCGCGCTTCTCTCCGGCAGAAACATTAACCACTTGTCCACTGA 2547

Qy 62 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 121
Db 2548 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2607

Qy 122 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 171
Db 2608 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2657

RESULT 3
US-08-702-344-26
: Sequence 26, Application US/08702344
: Patent No. 5723315
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John
: APPLICANT: Lavallee, Edward
: APPLICANT: Racie, Lisa
: APPLICANT: Merberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Spaulding, Vikki
: TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
: TITLE OF INVENTION: ENCODING THEM
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/702,344
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 144 base pairs
: TYPE: nucleic acid
```

```

: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-702-344-26

Query Match
Best Local Similarity 45.5%; Score 121.6; DB 1; Length 144;
Matches 127; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 31 AANAATAAACAACCTTATTATTCAGTGAATAAAAAAAAAAAAAAAAAAAAAA 90
Db 1 AAAAAAAAAAANTTTTATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 60

Qy 91 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 150
Db 61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120

Qy 151 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 171
Db 121 AAAAAAAAAAAAAAAAAAAAAA 141

RESULT 4
US-09-073-569-1
: Sequence 1, Application US/09073569
: Patent No. 6084088
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Grossmann, Angelika
: TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ZymoGenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/073,569
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sawislak, Deborah A.
: REGISTRATION NUMBER: 37,438
: REFERENCE/DOCKET NUMBER: 97-14
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-442-6672
: TELEFAX: 206-442-6678
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1733 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 34...1344
: OTHER INFORMATION:
: US-09-073-569-1

Query Match
Best Local Similarity 45.5%; Score 121.4; DB 3; Length 1733;
Matches 131; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```



```

? SEQUENCE CHARACTERISTICS:
? LENGTH: 2246 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? DESCRIPTION: /desc = "mouse PAL cDNA"
US-09-363-708-3

```

Query Match	43.6%	Score 116.4	DB 4	Length 2246
Best Local Similarity	83.0%	Pred. No. 1.2e-11		
Matches 132, Conservative	0	Mismatches 27	Indels 0	Gaps 0

[illegible]

RESULT 11
US-09-071-224-3
; Sequence 3, Application US/09071224

1 GENERAL INFORMATION:
2 APPLICANT: Lok, Si
3 APPLICANT: Presnell, Scott R.
4 APPLICANT: Jelmberg, Anna C.
5 APPLICANT: Gilbert, Teresa
6 APPLICANT: Foster, Donald C.
7 APPLICANT: Adams, Rodyn L.
8 APPLICANT: Lennie, Joyce M.
9 TITLE OF INVENTION: MAMMALIAN ZCYTOR5
10 NUMBER OF SEQUENCES: 37
11 CORRESPONDENCE ADDRESS:

```

; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
;

```

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Diskette
3  COMPUTER: IBM Compatible
4  OPERATING SYSTEM: DOS
5  SOFTWARE: FASTEO for Windows Version 2.0
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/09/071,224

```

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
```

ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-222
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:

```
; INFORMATION FOR SEQ ID NO: 3:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 1813 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
```

```

; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 88...1362
; OTHER INFORMATION:
;
US-09-071-224-3

```

Query Match	43.48;	Score 116;	DB 4;	Length 1813;
Best Local Similarity	86.58;	Pred. No. 1.4e-11;		
Matches 128; Conservative	0;	Mismatches 20;	Indels 0;	Gaps 0;

QY	1665	1725	1785
QY	34	94	154
Db	1665	1725	1785

RESULT 12
US-09-394-645-1
; Sequence 1, Application US/09394645

```

: GENERAL INFORMATION:
: APPLICANT: Sassetti, Christopher M.
: APPLICANT: Rosen, Steven R.
: TITLE OF INVENTION: Endoglycan: A NOVEL PROTEIN HAVING SELECTIN
: TITLE OF INVENTION: LIGAND AND CHEMOKINE PRESENTATION ACTIVITY
: FILE REFERENCE: 6510-1220S1
: CURRENT APPLICATION NUMBER: US/09/394,645
: CURRENT FILING DATE: 1999-09-13
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 2269
: TYPE: DNA
: ORGANISM: human
: OS-09-394-645-1

```

Query Match	43.28;	Score 115.4;	DB 4;	Length 2269;
Best Local Similarity	99.18;	Pred. No. 1.8e-11;		
Matches 116;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

RESULT 13

Sequence 1. Application US/09245560B
Patent No. 6395882
GENERAL INFORMATION:
Applicant: Rosen, Steven D.
Applicant: Sasselet, Christopher M.
TITLE OF INVENTION: No. 6395882el Selectin Ligands
FILE REFERENCE: UCL0097051
CURRENT APPLICATION NUMBER: US/09/243,560B
CURRENT FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: US 60/074,389
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1

```

; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-243-560B-1

```

Query Match	43.28	Score 115.4	DB 4	Length 2269
Best Local Similarity	99.18	Pred. No. 1.8e-11		
Matches 116	Conservative 0	Mismatches 1	Indels 0	Gaps 0

[illegible][illegible]

RESULT 14
US-09-247-373B-33
Sequence 33 Application US/00347373B

Patent NO. 6168954
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL.

```

: TITLE OF INVENTION: SUBSTRATE-DEPENDENT 5'-KINSEPHASE
:
: FILE REFERENCE: CL-1108-A
:
: CURRENT APPLICATION NUMBER: US/09/247, 373B
:
: CURRENT FILING DATE: 1999-02-10

```

```

; PRIOR FILING DATE: 1997-09-05
;
; NUMBER OF SEQ ID NOS: 56
;
; SOFTWARE: Microsoft Office 97

```

```
; LENGTH: 1117
;; TYPE: DNA
; ORGANISM: SOYBEAN
```

```

; NAME/KEY: unsure
; LOCATION: (1101)
; OTHER INFORMATION: M-A OR C
NAME/KEY:
LOCATION:
OTHER INFORMATION:

```

```

; LOCATION: (1104)
; OTHER INFORMATION: M=A OR C
; NAME/KEY: unsure
; LOCATION: (1115)

```

Query Match 42.6% Score 1
: OTHER INFORMATION: N=G or A or T or C
US-09-247-373B-33

2 CTTTCACCTTGTGTCAGATCCTCCACAGCCCCCGCAAAATAAATAAACCATTCCTTAATGGCTACACTGCA 61
 Best Local Similarity /8.2% Pred. NO. 3.1e-11;
 Matches 133; Conservative 2; Mismatches 35; Indels 0; Gaps 0;

[illegible][illegible]

Db 1063 AAAAAAAAAAAAAAAAAA CAAAAAAAAA MAAAAAAAAA 1112

US-09-443-041A-27
; Sequence 27, Application US/09443041A
; Patent No. 6465717

APPLICANT: Famodu, Omolayo O.
APPLICANT: Orozco, Buddy

```

; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:

```

; CURRENT FILING DATE: 1999-11-18
 ; PRIOR APPLICATION NUMBER: 60/109,283
 ; PRIOR FILING DATE: 1998-11-20

```

; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 1447

```

ORGANISM: Glycine max
US-09-443-041A-27

Matches	114;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

[illegible]

Dd 1374 AA 1428

```

search completed: match 21, 2003, 15:15:43
Job time : 42.166 secs

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100

Q:

120

```

Db 61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120
Qy 121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGG 180
Db 121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGG 180
Qy 181 GGGGGGGGGGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 240
Db 181 GGGGGGGGGGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 240
Qy 241 AAAAAAAAAAGAGAGAAANNCNTTGTAT 267
Db 241 AAAAAAAAAAGAGAGAAANNCNTTGTAT 267

RESULT 2
US-09-893-238-10
: Sequence 10, Application US/09893238
: Patent No. US20020150973A1
: GENERAL INFORMATION:
: APPLICANT: Moore, K.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
: FILE REFERENCE: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
: CURRENT APPLICATION NUMBER: US/09/893,238
: PRIOR FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: 09/245,041
: PRIOR FILING DATE: 1999-02-05
: PRIOR APPLICATION NUMBER: 60/093,630
: PRIOR FILING DATE: 1998-07-21
: PRIOR APPLICATION NUMBER: 60/104,978
: NUMBER OF SEQ ID NOS: 129
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 1051
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-893-238-10

Query Match 49.4%; Score 131.8; DB 10; Length 1051;
Best Local Similarity 82.5%; Pred. No. 3.7e-08;
Matches 151; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 85
Qy 121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGG 180
Db 86 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAGGGG 145
Qy 181 GGGGGGGGGGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 240
Db 146 GAAGGGGAGCGCGCTGTGTATGTTCGTGGGGCGCGCTCAAGCCCAAGA 205
Qy 241 AAA 243
Db 206 AGA 208

RESULT 3
US-10-091-483-131
: Sequence 131, Application US/10091483
: Publication No. US20030049650A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT12C1
: CURRENT APPLICATION NUMBER: US/10/091,483
: CURRENT FILING DATE: 2002-03-07
: NUMBER OF SEQ ID NOS: 348

```

```

: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 131
: LENGTH: 698
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (687)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (688)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (692)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (696)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (698)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-091-483-131

Query Match 46.7%; Score 124.6; DB 9; Length 698;
Best Local Similarity 87.2%; Pred. No. 2.7e-07;
Matches 136; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 21 TAGAGCCCTGAAATATTAACACACTTATTTATCCAGTGAATAAAAAAAAAAAAAA 80
Db 531 TGAGACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 590
Qy 81 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 140
Db 591 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 650
Qy 141 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGG 176
Db 651 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGG 686

RESULT 4
US-09-764-846-131
: Sequence 131, Application US/09764846
: Patent No. US20020102638A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT1212
: CURRENT APPLICATION NUMBER: US/09/764,846
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 131
: LENGTH: 698
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (687)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (688)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (692)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (696)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (698)

```

```

RESULT 6
US-09-960-352-13342/C
: Sequence 13342, Application US/09960352
: Patent No. US20020137139A1
: GENERAL INFORMATION:
:
: APPLICANT: Warren, Wesley C.
:
: APPLICANT: Tao, Nengbing
:
: APPLICANT: Byatt, John C.
:
: APPLICANT: Mathialagan, Nagappan
:
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
:
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
:
: FILE REFERENCE: 16511.006/37-21(10298)C
:
: CURRENT APPLICATION NUMBER: US/09/960,352
:
: CURRENT FILING DATE: 2001-09-24
:
: NUMBER OF SEQ. ID NOS: 15112
:
: SEQ. ID NO 13342

```

RESULT 8
US-09-726-643-35

```
; Sequence 35, Application US/09726643
; Patent No. US20020028449A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/09/726,643
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,725
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 35
; LENGTH: 3466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3462)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (3466)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-09-726-643-35
```

```
Query Match          46.2%; Score 123.4; DB 10; Length 3466;
Best Local Similarity 91.5%; Pred. No. 3.2e-07;
Matches 130; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 30 GAANAATTAACAACTTATTTCACAGTCAGTCAAAAAAAAAAAAAAAAAAAAAA 89
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3312 GCAGAAATTAATTTCTTAGCTATTCAGCAAAAAAAAAAAAAAAAAAAAAA 3371
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 90 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 149
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3372 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3431
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 150 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 171
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3432 AAAAAAAAAAAAAAAAAAAAAAA 3453
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 9
US-09-960-352-5566
; Sequence 5566, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengding
; APPLICANT: Byate, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298YC
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5566
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-LIB3058-010-Q1-K1-F7
US-09-960-352-5566
```

```
Query Match          46.0%; Score 122.8; DB 10; Length 383;
Best Local Similarity 88.1%; Pred. No. 4.5e-07;
Matches 133; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
```

```
QY 29 TGAANAATTAACAACTTATTTCACAGTCAAAAAAAAAAAAAAAAAAAAAA 88
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 111 TCAAAATTAATTCACACAGATGTAAAAAAGGAGGAGGAGGAGGAGGAGGAGG 170
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
QY 89 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 148
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 171 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 230
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 149 AAAAAAAAAAAAAAAAAAAAAAGGGGGG 179
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 231 AAAAAAAAAAAAAAAAAAAAAAGGGGGG 261
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 10
US-10-091-483-105
; Sequence 105, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212C1
; CURRENT APPLICATION NUMBER: US/10/091,483
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 105
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (612)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (620)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (621)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-091-483-105
```

```
Query Match          45.6%; Score 121.8; DB 9; Length 621;
Best Local Similarity 87.4%; Pred. No. 5.7e-07;
Matches 132; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 29 TGAANAATTAACAACTTATTTCACAGTCAAAAAAAAAAAAAAAAAAAAAA 88
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 469 TTATCTATTGCAAAAGATATTCAACCTAAAAAAGGAGGAGGAGGAGGAGGAGG 528
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 89 AAAAAAAAAAAAAAAAAAAAAAGGGGGG 179
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 529 AAAAAAAAAAAAAAAAAAAAAAGGGGGG 179
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 149 AAAAAAAAAAAAAAAAAAAAAAGGGGGG 179
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 589 AAAAAAAAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 619
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 11
US-09-764-846-105
; Sequence 105, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 105
```

Query Match 45.5%; Score 121.6; DB 9; Length 144;

```

? Patent No.: US20020090672A1
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: P1206
? CURRENT APPLICATION NUMBER: US/09/764,853
? CURRENT FILING DATE: 2001-01-17
? PRIOR APPLICATION date removed - consult PALM or file wrapper
? NUMBER OF SEQ ID NOS: 939
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 161

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 16:21:58 ; Search time 1284.89 Seconds
(without alignments)
3365.420 Million cell updates/sec

Title: US-09-823-101-9
Perfect score: 267
Sequence: 1 actcaccgtctcagctc.....aagagayaaancttcat 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba:*
2: em_esthum:*
3: em_estinu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	163.2	61.1	943	17	AZ540199 ENT0014TR
C 2	158.4	59.3	870	17	BH157873 ENT0014TR
C 3	156.8	58.7	902	17	AZ546010 ENT0014TR
C 4	155.2	58.1	500	9	AL640113 AL640113
C 5	152.2	57.0	824	17	BH159193 ENT0014TR
C 6	152	56.9	911	17	AZ682313 ENT0014TR

Result No.	Score	Query Match	Length	ID	Description
C 7	150.4	56.3	968	17	AZ682070 ENT0014TR
C 8	148.6	55.7	971	17	BH156534 ENT0014TR
C 9	147.2	55.1	901	13	BM415391
C 10	147	55.1	513	9	AL640575
C 11	146.8	55.0	589	9	AL639664
C 12	146.6	54.9	508	9	AL640416
C 13	144.6	54.2	324	13	B364338
C 14	144.4	54.1	517	9	AL644467
C 15	144.2	54.0	1011	14	BQ954179
C 16	142.2	53.3	340	9	AL642885
C 17	141.8	53.1	538	14	BQ250313
C 18	141.6	53.0	937	17	AZ545521
C 19	140.8	52.7	516	12	BF682838
C 20	139.8	52.4	514	14	BF680776
C 21	139.4	52.2	302	10	BE684807
C 22	138.4	52.2	384	12	BG107847
C 23	138.4	51.8	1630	12	BG110241
C 24	138.2	51.8	1081	13	BM416124
C 25	137.6	51.5	782	13	B1861670
C 26	137.4	51.5	194	13	B1370638
C 27	137	51.3	722	12	BF138605
C 28	137	51.3	999	17	CNS047NK
C 29	136.4	51.1	256	9	AL644237
C 30	136.2	51.0	782	10	BE612435
C 31	136	50.9	896	17	CNS00BP8
C 32	135.8	50.9	523	9	AL514015
C 33	135.8	50.9	858	13	BM415483
C 34	135.8	50.9	884	17	BH162006
C 35	135.6	50.8	368	12	BG732549
C 36	135.4	50.7	449	10	BE619240
C 37	135.4	50.7	674	12	BG620859
C 38	135.4	50.7	829	12	BF970658
C 39	135.2	50.6	401	12	BG108147
C 40	135	50.6	411	12	BF348329
C 41	134.4	50.3	716	12	BE013113
C 42	134.4	50.3	687	12	BG284822
C 43	134.2	50.3	171	12	BF339594
C 44	134.2	50.3	1101	17	CNS017V6
C 45	134	50.2	515	12	BG622615

ALIGNMENTS

RESULT 1
LOCUS AZ540199 943 bp DNA linear GSS 14-NOV-2000
DEFINITION ENT0014TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
ACCESSION AZ540199
VERSION AZ540199.1 GI:11146774
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica.
REFERENCE 1 (bases 1 to 943)
Eukaryota: Entamoebidae; Entamoeba.
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 15
High quality sequence stop: 261.


```

/organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_1fb="Entamoeba
histolytica Sheared DNA
Site_1: Bst I. Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,

```


BASE COUNT	179 a	161 c	101 g	527 t
ORIGIN				

31 AANATAAACCACTTATTTATCCAGTGAAAAAAAAAAAAAAAAAAAA 90

OY 91 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 150

QY 151 AAAAAAAAAAAAAAGGGGGGGGGGGGGGGGGGGA3GGGGGGGGGGGGGGG 210

QY 211 GGGGGGGGGCG 223

RESULT 8

ACCESSION	BH156534	
VERSION	BH156534.1	GI:15729545
REVISION	000	

ORGANISM	REFERENCE
<i>Entamoeba histolytica</i>	1 (bacc 145-071)
Eukaryota; Entamoebidae; Entamoeba	

TITLE
 Determination of clone end sequences from Entamoeba histolytica
 HMI:IMSS sheared DNA library (2001)
 Investigated (2001)

Department of Eukaryotic Genomics
The Institute for Genomic Research
0713 Medical Center Drive, Bethesda, MD 20895
ronn@igb.rockefeller.edu

Fax: 501 650 5543
Email: bjloftus@tiqr.org

```
seq primer: M13-Reverse
Class: shotgun
high qual: sequence start: 13
```

1. .971

```

/uu_ate1= caaou.0755
/clone_lib="Entamoeba histolytica sheared DNA"
/pato="Vector: pUC19 site 1. Pat 1. Constructed at mbe

```

genomic DNA isolated from bivalvular larvae of *E. histolytica* using a method described by Clark and Diamond (Clark, 1967) and Diamond (1967). Extrachloral histolysis of

C.8.7) and Diamond, D.3. (1999) *Encarnadas histocytica*: a method for isolate identification. Exp. Parasitol. 77:450. The DNA was mechanically sheared to give a

BASE COUNT	158 a	339 c	113 g	361 t
ORIGIN				

Qy 61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120

QY 121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGG 180

[illegible]

RESULT 9

DEFINITION OP21483 Mixed Stage EST's from *Globodera pallida*, the potato cyst nematode *Globodera pallida* cDNA, mRNA sequence.

KEYWORDS	EST.
SOURCE	Globodera pallida.

Tylenchoidea; Heteroderidae; Heteroderinae; Globodera
1 (bases 1 to 901)

JOURNAL Unpublished (2001)
COMMENT Contact: Opperman, C

Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.6699

PCNGT11-3_F_D08_PCN_F_062.abl
Location/Qualifiers

```
/organism="Globodera pallida"  
/db_xref="taxon:36090"
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```
/note="Vector: lambda Gill; This is a collaborative effort
between IACR-Rothamsted and North Carolina State
```

	IACR-Kolnamssted."			
BASE COUNT	323 a	135 c	313 g	129 t
others				1 others

Query match	55.18;	score 147.2;	DB 13;	length 901;
Best Local Similarity	85.08;	Pred. No. 3.6e-06;		

31 AANAMTAAAAACACCTATTTTATCCAGTCAAAAAAAAAAAAAAAAAAAAAA 90

```
D0      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 80
```

[illegible]

RESULT	10
AL640575	
LOCUS	
DEFINITION	AL640575 XGC-neurula Silurana tropicalis cDNA clone TNeu003a21 5'
ACCESSION	AL640575
VERSION	AL640575.1
KEYWORDS	GI:16792706
SOURCE	EST.
ORGANISM	western clawed frog. Silurana tropicalis Euryzoia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae; Xenopodinae; Silurana. 1 (bases 1 to 513)
REFERENCE	Huckie,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10-2001) Unpublished (2001) Contact: Huckie E
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

Location/Qualifiers

1..513

FEATURES

Source

```

/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu003821"
/clone_1fb="Xgc-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/vector="PCSI07; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from neurula
EcoRI-NotI cut cDNA was then ligated into pCSI07 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT      219 a      90 c      98 g      100 t      6 others
ORIGIN

```

[illegible]

RESULT	11
AL639664	
LOCUS	589 bp mRNA linear EST 12-DEC-2001
DEFINITION	AL639664 XGC-neurula Silurana tropicalis cDNA clone TNeu01lp1 5',
ACCESSION	mRNA sequence.
VERSION	AL639664
KEYWORDS	AL639664.1 GI:16791795
SOURCE	EST.
ORGANISM	western clawed frog.
	Silurana tropicalis
	Euryptera; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
	Xenopodinae; Silurana.
REFERENCE	1 (bases 1 to 589)
AUTHORS	Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE	Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL	Unpublished (2001)
COMMENT	Contact: Huckle E

This sequence is from a Xenopus Gene Collection (xgc) library
 constructed by Aaron M. Zorn.
 Location/Qualifiers
 1..589
FEATURES
 source .

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/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu011p01"
/clone_11b="Xgc-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/notes="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from neurula
EcoRI-NotI cut cDNA was then ligated into pcs107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT      224 a      113 c      117 g      133 t      2 others
ORIGIN

```

Query Match	55.0%	Score 146.8;	DB 9,	Length 589;
Best Local Similarity	80.0%	-Pred. No. 5.3e-06;		
Matches 172; Conservative	0;	Mismatches 43;	Indels 0;	Gaps 0

OY	34	AAAAAAAAACAATTCTTTTATCCAGTGAAAAA	93
Db	213	AAATGAAAATAAGATTAACTCAGACAGAAAAA	272
OY	94	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	153
Db	273	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	332
OY	154	AAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGA	213
Db	333	AAAAAAAAAAAAAAAAAANGGGGGGGGGGGGCC	392
OY	214	GGGGGGGGCCCCCCCCCCCCCAAAACAAA	248
Db	393	GGGGGTTTTTCCTCCCCTCCCAAAAAAAA	427

RESULT	12
AL640416	
LOCUS	508 bp mRNA linear EST 12-DEC-2001
DEFINITION	AL640416 XGC-neurula <i>Silurana tropicalis</i> cDNA clone tneuo02b22 5'
ACCESSION	AL640416 mRNA sequence.
VERSION	AL640416
KEYWORDS	AL640416.1 GI:16792547
SOURCE	EST.
ORGANISM	western clawed frog. <i>Silurana tropicalis</i>

REFERENCE	TITLE	AUTHORS	JOURNAL	COMMENT
1 (bases 1 to 508)				
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.W. and Rogers,J.				
Sanger Xenopus tropicalis EST project 2001 (10-2001)				
Unpublished (2001)				
Contact: Huckle E				

Hinxton, Cambridgeshire, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu02b22.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

```

/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Neu002b22"
/clone_1id="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/notice="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5' end of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT      206 a      92 c      77 g      131 t      2 others
ORIGIN

```

Query Match	54.9%	Score 146.6	DB 9	Length 508
Best Local Similarity	78.6%	Pred. No. 6.2e-06		
Matches 173	Conservative 0	Mismatches 47	Indels 0	Gaps 0

QY	32	ANATATTAACACACTATTATTATTCACGAGAAAAA	91
Db	141	ACATTAAACAAAAA	200
QY	92	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	151
Db	201	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	260
QY	152	AAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGAG	211
Db	261	AAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGCC	320
QY	212	GGGGGGGGGCGCGCCCGCCCGCCCAAAACA	251
Db	321	TGGGGGGGCGCCCGCCCGCCCGCCCAAAAAA	360

RESULT 13	LOCUS	DEFINITION
BJ364338	324 bp	mRNA, linear
BJ364338	Dictyostelium discoideum cDNA library, CP	Dictyostelium discoideum cDNA clone ddc3112 5', mRNA sequence.

KEYWORDS	EST.
SOURCE	dictyostelium discoideum.
ORGANISM	dictyostelium discoideum.
REFERENCE	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
AUTHORS	1 (bases 1 to 324)
TITLE	Utsunishihara,H., Tanaka,Y., Kohara,Y. and Shir-i,T. Full length cDNA of dictyostelium discoideum at the culmination stage
JOURNAL	unpublished (2002)
COMMENT	Contact : Tadasu Shin-1

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856

Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
Location/Qualifiers
1. .324

```

/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc3112"
/clone_1lb="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
/dev_stage="Culmination stage"
BASE COUNT      160 a      27 c      73 g      43 t      21 others
ORIGIN

```

Query Match	54.2%	Score 144.6	DB 13	Length 324
Best Local Similarity	97.6%	Pred. No. 1.3e-05		
Matches 150	Conservative 0	Mismatches 12	Indels 0	Gaps 0

[illegible]

RESULT 14	AL644467	LOCUS	DEFINITION
	AL644467	517 bp	mRNA
	AL644467	XGC-neurula	linear
		Silurana tropicalis	cDNA clone TNeu027n22 5',
		mRNA sequence.	

ACCESSION	AL644467
VERSION	AL644467.1
KEYWORDS	GI:167965922
SOURCE	EST.
ORGANISM	western clawed frog. Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae; Xenopodinae; Silurana.

REFERENCES
Huckie, E., Taylor, R., Ashurst, J. L., Zorn, A. M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckie E

Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu027n22.sp6
Sequencing primer: Sp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

```

/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu027n2"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107. Site_1: EcoRI. Site_2: NotI. cDNA
was oligo dt primed from 5ug of poly A+ RNA from neurula
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

```

BASE COUNT	213 a	111 c	84 g	109 t
ORIGIN				
Query Match	54.18; Score 144.4; DB 9; Length 517			

	Oy	40	AACACCTATTATTTATCCGCTGA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	99
	Dd	80	AAATTAATCTTGTTTAAATATA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	139
	Oy	100	AAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	159
	Dd	140	AAAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	199
	Oy	160	AAAAAAAAAAAAAGGGGGGGGGGGG	GAGGGGGGGGGGGGGGGGGG	219
	Dd	200	AAAAAAAAAAAAAGGGGGGGGGGGG	GGGGGGGGGGGGGGGGGGC	259
	Oy	220	GGCGCGCGCGCGCGCGCAAAACA	AAAAA	249
	Dd	260	TTTTTCCTCCCCCCCCCAAAAAA	AAA	289

RESULT 15	
B0954179	
LOCUS	
DEFINITION	B0954179 1011 bp mRNA linear EST 21-AUG-2002
	AGENCOURT_8803124 lupsk1.sciatlq.nerve Homo sapiens cDNA clone
	IMAGE:6199064 5', mRNA sequence.
ACCESSION	B0954170

VERSION	BQ954179.1	GI:22369657
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 1011)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: BLAN13611 row: 1 column: 09
High quality sequence stop: 206.

FEATURES
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:6199004"
/clone_1b="LupSKI_sclaticC.nerve"
/sex="male
/tissue_type="sclatic nerve"
/dev_stage="adult, 70 yr"

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5'-GACGATGTTTCAGACGCGACGCCCCCCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified, library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT	219 a	318 c	317 g	154 t	3 others
ORIGIN					

Query Match	54.08;	Score 144.2;	DB 14;	Length 1011;
Best Local Similarity	81.18;	Pred. No. 6.4e-06;		
Matches 167; Conservative	0;	Mismatches 39;	Indels 0;	Gaps 0;

Oy	28	CTGANNATTTAAAAACCACTTATTTTTATTCAGTGAAAAAAAAAAAAAAAAAA	87
Db	31	CTACTGATTTAACTGSACTTAAAAGCATCAAAAAAAAAAAAAAAAAA	90
Oy	88	AA	147
Db	91	AA	150
Oy	148	AAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGAGGAGGGGGGGG	207
Db	151	AAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGCTTCCCTGGGC	210
Oy	208	GGGGGGGGGGGGCGGCCCCCCC	233
Db	211	GGGGGGGGCCCTTCCCCCTCCC	236

Search completed: March 21, 2003, 19:11:36
Job time : 1296.09 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 11:56:08 ; Search time 3525.69 Seconds

(without alignments)
4490.451 Million cell updates/sec

Title: US-09-823-101-10

Perfect score: 544
Sequence: 1 accacaatggtattataaagg.....tccttacagtgacatagca 544

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vi: *
30: em_htg_hum: *
31: em_htg_in: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rtd: *
36: em_htg_man: *
37: em_htg_vrl: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. NO. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	100.0	544	6 AX338097	AX338097 Sequence
2	49.4	9.1	360	6 AX340067	AX340067 Sequence
3	49.4	9.1	377	6 AX339767	AX339767 Sequence
4	49.4	9.1	410	6 AX381356	AX381356 Sequence
5	49.4	9.1	544	6 AX341339	AX341339 Sequence
6	49.4	9.1	1114	6 AR030953	AR030953 Sequence
7	49.4	9.1	1114	6 AR100599	AR100599 Sequence
8	49.4	9.1	1114	6 AX193504	AX193504 Sequence
9	49.4	9.1	1114	6 AX193507	AX193507 Sequence
10	49.4	9.1	1130	6 AY007243	AY007243 Homo sapi
11	49.4	9.1	1200	9 AF254415	AF254415 Homo sapi
12	49.4	9.1	168018	2 AL592186	AL592186 Homo sapi
13	49.4	9.1	176704	2 AC013703	AC013703 Homo sapi
14	48.4	8.9	374	6 AX351272	AX351272 Sequence
15	48.4	8.9	476	6 AX341943	AX341943 Sequence
16	48.4	8.9	554	6 AX381524	AX381524 Sequence
17	47.8	8.8	309	6 AX340507	AX340507 Sequence
18	47.8	8.8	466	6 AX340889	AX340889 Sequence
19	47.8	8.8	533	6 AX340957	AX340957 Sequence
20	47.8	8.8	544	6 AX340060	AX340060 Sequence
21	47.8	8.8	549	6 AX192930	AX192930 Sequence
22	47.8	8.8	1152	6 AX193505	AX193505 Sequence
23	47.8	8.8	1161	9 AF345934	AF345934 Homo sapi
24	47.8	8.8	1192	9 BC017089	BC017089 Homo sapi
25	47.8	8.8	137955	9 AL359752	AL359752 Human DNA
26	47.4	8.7	78	6 AX192757	AX192757 Sequence
27	45.8	8.4	260	6 AX379256	AX379256 Sequence
28	42.4	7.8	7218	6 166494	166494 Sequence 14
29	41.6	7.6	20130	10 AF211347	AF211347 Mus muscu
30	41.6	7.6	299880	2 AC127308	AC127308 Mus muscu
31	41.4	7.6	254336	10 AC098838	AC098838 Genomic S
32	40.4	7.4	129988	2 AC127961	AC127961 Rattus no
33	40	7.4	1060	6 E52142	E52142 TSA7005 gen
34	39.4	7.2	165124	2 AC110371	AC110371 Rattus no
35	39	7.2	34410	3 AC008242	AC008242 Leishmani
36	39	7.2	69894	2 AC123604	AC123604 Mus muscu
37	39	7.2	92500	2 AC098845	AC098845 Leishmani
38	39	7.2	116000	2 AC129714	AC129714 Leishmani
39	38.6	7.1	215874	2 AC102124	AC102124 Mus muscu
40	38.2	7.0	185319	2 AC110364	AC110364 Rattus no
41	38.2	7.0	219031	2 AC094780	AC094780 Rattus no
42	38	7.0	334520	1 AP003588	AP003588 Nostoc sp
43	37.8	6.9	196693	2 AC098530	AC098530 Rattus no
44	37.6	6.9	146000	2 AP005433	AP005433 Homo sapi
45	37.6	6.9	194914	2 AC114359	AC114359 Rattus no

ALIGNMENTS

RESULT 1
AX338097
LOCUS AX338097 544 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 10 from Patent WO0175169.
ACCESSION AX338097
VERSION AX338097.1 GI:18128728
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Pluta, J., Chen, S.Y., Hu, P., Recipon, H. and Macina, R.A.
TITLE Compositions and methods for diagnosing, monitoring, staging, imaging and treating stomach cancer

JOURNAL	Patent: WO 0175169-A 10 11-OCT-2001;
Diadexus, Inc. (US)	
FEATURES	Location/Qualifiers
Source	1. 544 /Organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	150 a 134 c 142 g 118 t
ORIGIN	
Query Match	100.0%; Score 544; DB 6; Length 544;
Best Local Similarity	100.0%; Pred. No. 2,3e-165;
Matches 544; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ACACATGTTTATTAAAGATGTATGGCCACATCAACCAAGAGGATTTCTACATG 60
Db	1 ACACATGTTTATTAAAGATGTATGGCCACATCAACCAAGAGGATTTCTACATG 60
QY	61 GTAAGCCCTTCCTATGTGCGCAAGAGAAGAAACAGACATGGAGTTGGACGTGGTAGGT 120
Db	61 GTAAGCCCTTCCTATGTGCGCAAGAGAAGAAACAGACATGGAGTTGGACGTGGTAGGT 120
QY	121 GGTGGGTGTGCACGGCAGATGAGAGAAGAGGCGATGAAGGGTCTGTAGAAGCCATGAATGG 180
Db	121 GGTGGGTGTGCACGGCAGATGAGAGAAGAGGCGATGAAGGGTCTGTAGAAGCCATGAATGG 180
QY	181 GGGTTTAGAATGCTTGGATGTAGATTTCATGTTACACTAGCGCTGTATTCTCTGGGTGTAC 240
Db	181 GGGTTTAGAATGCTTGGATGTAGATTTCATGTTACACTAGCGCTGTATTCTCTGGGTGTAC 240
QY	241 AATTGCTTAATCCGGCGTCACACATTCGCCAGACCAACATCTGATGCGCAATCCAGTGACAG 300
Db	241 AATTGCTTAATCCGGCGTCACACATTCGCCAGACCAACATCTGATGCGCAATCCAGTGACAG 300
QY	301 CTGGATTACGACAGCAGCAATTCACAGAGCTGGCTGCTCTCCTTTATGACACAGACCTATC 360
Db	301 CTGGATTACGACAGCAGCAATTCACAGAGCTGGCTGCTCTCCTTTATGACACAGACCTATC 360
QY	361 AGGCGTACCCTGTCTTGGCTCTCTGGTACACGCCAATTCGCAAGCGCTACTTATGTAACAC 420
Db	361 AGGCGTACCCTGTCTTGGCTCTCTGGTACACGCCAATTCGCAAGCGCTACTTATGTAACAC 420
QY	421 ACGGGCAGCTGATTATACAGGACTCAACCCAGGCCAAACCCCTACCTATATCTATAG 480
Db	421 ACGGGCAGCTGATTATACAGGACTCAACCCAGGCCAAACCCCTATATCTATAG 480
QY	481 ACGGGCAGTTTGCACGGACGATCGCTCTGAGCTCCAGCAGCTCTTAAACAGTGACAT 540
Db	481 ACGGGCAGTTTGCACGGACGATCGCTCTGAGCTCCAGCAGCTCTTAAACAGTGACAT 540
QY	541 AGCA 544
Db	541 AGCA 544
RESULT 2	
AX340067	AX340067 360 bp DNA Linear PAT 10-JAN-2002
LOCUS	
DEFINITION	Sequence 314 from Patent WO0196388.
ACCESSION	AX340067
VERSION	
KEYWORDS	AX340067.1 GI:18136048
ORGANISM	human.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Jiang, Y., Harlocker, S.L. and Secrist, H.
TITLE	Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL	Patent: WO 0196388-A 314 20-DEC-2001;
FEATURES	CORIXA CORPORATION (US)
Source	Location/Qualifiers
	1. 360

BASE COUNT	104 a	67 c	108 g	79 t	2 others
ORIGIN					
Query Match	9.1%	Score 49.4;	DB 6;	Length 360;	
Best Local Similarity	72.9%	Pred. No. 0.00014;			
Matches	78;	Conservative	0;	Mismatches 26;	Indels 3; Gaps 1;
OY	1	ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCAAGCAAGGATTCATACATG	60		
DB	1	ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCTAGCAAG--ATTCTACT	57		
OY	61	GTAAGCCTTCCTATGTGCCAAGAGAGAAACAAGCATGGAGTTG	107		
DB	58	GGTAAACCTTCCTATGTGCCAAGAGAGAAACAAGCATGGAGTTG	104		
RESULT 3					
LOCUS	AX339767	377 bp	DNA	linear	PAT 10-JAN-2002
DEFINITION	Sequence 14 from Patent WO0196388.				
ACCESSION	AX339767				
VERSION	AX339767.1	GI:18135748			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	Jiang, Y., Harlocker, S. L. and Secrist, H.				
JOURNAL	Compositions and methods for the therapy and diagnosis of colon				
FEATURES	Cancer				
source	Patent: WO 0196388-A 14 20-DEC-2001;				
ORIGIN	CORIXA CORPORATION (US)				
BASE COUNT	109 a	71 c	110 g	85 t	2 others
Query Match	9.1%	Score 49.4;	DB 6;	Length 377;	
Best Local Similarity	72.9%	Pred. No. 0.00014;			
Matches	78;	Conservative	0;	Mismatches 26;	Indels 3; Gaps 1;
OY	1	ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCAAGGATTCATACATG	60		
DB	1	ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCTAGCAAG--ATTCTACT	57		
OY	61	GTAAGCCTTCCTATGTGCCAAGAGAGAAACAAGCATGGAGTTG	107		
DB	58	GGTAAACCTTCCTATGTGCCAAGAGAGAAACAAGCATGGAGTTG	104		
RESULT 4					
LOCUS	AX381356	410 bp	DNA	linear	PAT 18-MAR-2002
DEFINITION	Sequence 294 from Patent WO0212280.				
ACCESSION	AX381356				
VERSION	AX381356.1	GI:19576175			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	Pyle, R. A., Xu, J. and Secrist, H.				
JOURNAL	Compositions and methods for the therapy and diagnosis of colon				
FEATURES	Cancer				
source	Patent: WO 0212280-A 294 14-FEB-2002;				
ORIGIN	CORIXA CORPORATION (US)				
BASE COUNT	109 a	71 c	110 g	85 t	2 others

BASE COUNT	288 a	291 c	262 g	273 t
ORIGIN				
Query Match		9.1%;	Score 49.4;	DB 6;
Best Local Similarity		72.9%;	Pred. No. 0.00015;	Length 1114;
Matches 78;	Conservative	0;	Mismatches 26;	Indels 3;
				Gaps 1;
OY	1	ACACAATGCTTTATTAAAGAAATGTATGGCCACATCAACCAAGCAAGGATTTACATG	60	
Db	1112	ACACAATGCTTTATTAAAGAAATGTATGGCCACATCAACCAAGCAAGGATTTACATG	1056	
OY	61	GTTAAAGCCTTCCTATGTGCCAAGAGAGAAACAGACGATGGAGTTG	107	
Db	1055	GGTAAACCTTCCTATGTGCCAAGAGAGAAACAGACGATGGAGTTG	1009	
RESULT 7				
LOCUS	ARI00599/c		1114 bp	DNA
DEFINITION	Sequence 1 from patent US 6080722.			linear
ACCESSION	ARI00599			PAT 14-FEB-2001
VERSION	ARI00599.1	GI:12811047		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1114)			
TITLE	Soppet,D.R., Li,Y. and Dillon,P.J.			
JOURNAL	Colo specific gene and protein			
FEATURES	Patent: US 6080722-A 1 27-JUN-2000;			
	Location/Qualifiers			
	1..1114			
BASE COUNT	288 a	291 c	262 g	273 t
ORIGIN				
	/organism="unknown"			
Query Match		9.1%;	Score 49.4;	DB 6;
Best Local Similarity		72.9%;	Pred. No. 0.00015;	Length 1114;
Matches 78;	Conservative	0;	Mismatches 26;	Indels 3;
				Gaps 1;
OY	1	ACACAATGCTTTATTAAAGAAATGTATGGCCACATCAACCAAGCAAGGATTTACATG	60	
Db	1112	ACACAATGCTTTATTAAAGAAATGTATGGCCACATCAACCTTACGACAGG--ATTCTACT	1056	
OY	61	GTTAAAGCCTTCCTATGTGCCAAGAGAGAAACAGACGATGGAGTTG	107	
Db	1055	GGTAAACCTTCCTATGTGCCAAGAGAGAAACAGACGATGGAGTTG	1009	
RESULT 8				
LOCUS	AXI93504/c		1114 bp	DNA
DEFINITION	Sequence 1071 from Patent WO0149716.			linear
ACCESSION	AXI93504			PAT 15-AUG-2001
VERSION	AXI93504.1	GI:15211444		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1114)			
AUTHORS	Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J.,			
TITLE	Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.			
JOURNAL	Compounds for immunotherapy and diagnosis of colo cancer and			
	Methods for their use			
	Patent: WO 0149716-A 1071 12-JUL-2001;			
FEATURES	CORIXA CORPORATION (US)			
	Location/Qualifiers			
	1..1114			
BASE COUNT	288 a	291 c	262 g	273 t
ORIGIN				
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			

Query Match 9.1%; Score 49.4; DB 6; Length 1114;
Best Local Similarity 72.9%; Pred. No. 0.00015;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTCATCANG 60
DB 1112 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTCATCANG 60
QY 61 GTAAACCTTCTATGTCAGAGAAACAGAGCATGAGTTG 107
DB 1055 GTAAACCTTCTATGTCAGAGAAACAGAGCATGAGTTG 1009

RESULT 9
AX193507/c 1114 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 1074 from Patent WO0149716.
ACCESSION AX193507
VERSION AX193507.1 GI:15211447
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J.,
Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.
Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
Patent: WO 0149716-A 1074 12-JUL-2001;
JOURNAL CORIXA CORPORATION (US)
TITLE Location/Qualifiers
FEATURES
source 1. 1114
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 288 a 291 c 262 g 273 t
ORIGIN

Query Match 9.1%; Score 49.4; DB 6; Length 1114;
Best Local Similarity 72.9%; Pred. No. 0.00015;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTCATCANG 60
DB 1112 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTCATCANG 60
QY 61 GTAAACCTTCTATGTCAGAGAAACAGAGCATGAGTTG 107
DB 1055 GTAAACCTTCTATGTCAGAGAAACAGAGCATGAGTTG 1009

RESULT 10
AY007243/c 1130 bp mRNA linear PRI 23-APR-2001
LOCUS AY007243
DEFINITION Homo sapiens regenerating gene type IV mRNA, complete cds.
ACCESSION AY007243
VERSION AY007243.1 GI:12621025
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE Hartuppe,J.C., Zhang,H., Bonaldo,M.F., Soares,M.B. and
Dilekgraeffe,B.K.
Isolation and characterization of a cDNA encoding a novel member of
the human regenerating protein family: Reg IV
JOURNAL Blochim. Biophys. Acta 1518 (3), 287-293 (2001)
MEDLINE 21210973
PUBMED 11311942
REFERENCE 2 (bases 1 to 1130)
AUTHORS Dilekgraeffe,B.K., Hartuppe,J.C., Zhang,H., Soares,M.B. and

TITLE Bonaldo,M.F.
JOURNAL Direct Submission
Submitted (18-AUG-2000) Gastroenterology, Washington University
School of Medicine, 660 S. Euclid Ave., Campus Box 8124, St. Louis,
MO 63110, USA
FEATURES
source Location/Qualifiers
1. 1130
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
123..599
/note="RegIV"
/codon_start=1
/product="regenerating gene type IV"
/protein_id="AA02562.1"
/db_xref="GI:12621026"
/translation="MASRSMRLLLSLCAKTGVLDIIMRSCAPGWYHKSNCYG
FKRLNWSDALEECOSYNGAHLASILSLKEASTIAETISGYORSOPWIGLHDPQR
QOMWIDGAMLYRSMGSKMGKNCHEMSNNNPLTWSNCKRQHFICKYRP"
BASE COUNT 291 a 293 c 265 g 281 t
ORIGIN

Query Match 9.1%; Score 49.4; DB 9; Length 1130;
Best Local Similarity 72.9%; Pred. No. 0.00015;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTCATCANG 60
DB 1124 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTCATCANG 60
QY 61 GTAAACCTTCTATGTCAGAGAAACAGAGCATGAGTTG 107
DB 1067 GTAAACCTTCTATGTCAGAGAAACAGAGCATGAGTTG 1021

RESULT 11
AF254415 1200 bp mRNA linear PRI 01-MAY-2001
LOCUS AF254415/c
DEFINITION Homo sapiens gastrointestinal secretory protein GISP mRNA, complete
cds.
ACCESSION AF254415
VERSION AF254415.1 GI:13897565
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1200)
AUTHORS Lin,W.-C.
TITLE Identification of gastrointestinal secretory protein (GISP), a new
member of lithostathine gene family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1200)
AUTHORS Lin,W.-C.
TITLE Direct Submission
Submitted (09-APR-2000) Institute of Biomedical Sciences, Academia
Sinica, No. 128 Academia Road, Taipei 115, Taiwan
FEATURES
source Location/Qualifiers
1. 1200
/organism="Homo sapiens"
/db_xref="taxon:9606"
182..658
/codon_start=1
/product="gastrointestinal secretory protein GISP"
/protein_id="AAK48435.1"
/db_xref="GI:13897566"
/translation="MASRSMRLLLSLCAKTGVLDIIMRSCAPGWYHKSNCYG
FKRLNWSDALEECOSYNGAHLASILSLKEASTIAETISGYORSOPWIGLHDPQR
QOMWIDGAMLYRSMGSKMGKNCHEMSNNNPLTWSNCKRQHFICKYRP"
BASE COUNT 324 a 304 c 283 g 289 t
ORIGIN

Query Match 9.1%; Score 49.4; DB 9; Length 1200;

Best Local Similarity 72.9%; Pred. No. 0.00015;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 ACACATGCTTTATTAAAGCATGTATGCCCATCATACCAAGCAAGGATTCTACATG 60

Db 1183 ACACATGCTTTATTAAAGCATGTATGCCCATCATACCAAGGATTCTACATG 1127

QY 61 GTAAGCGCTTCCTATGCGCAAGAGAAACAGACAGCATGAGTGTG 107

Db 1126 GGTAAACCTTCCTATGCGCAAGAGAAACAGACAGCATGAGTGTG 1080

RESULT 12

AL592186/c 168018 bp DNA linear HTG 29-JUL-2001

LOCUS Homo sapiens chromosome 1 clone RP11-136A14, *** SEQUENCING IN

DEFINITION PROGRESS ***, 4 unordered pieces.

ACCESSION AL592186

VERSION AL592186.2 GI:14575479

KEYWORDS HTG: HTGS_PHASE1; HTGS_CANCELLED.

SOURCE

ORGANISM

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 168018)

REFERENCE Submitted (28-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,

AUTHORS CB10 ISA, UK. E-mail enquiries: humquerry@sanger.ac.uk

JOURNAL requests: clonequest@sanger.ac.uk

On Jun 28, 2001 this sequence version replaced gi:14530324.

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquerry@sanger.ac.uk

----- Project Information

Center project name: ba136A14

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 167348 bases at least 940

Consensus quality: 167504 bases at least 930

Consensus quality: 167612 bases at least 920

Insert size: 167718; sum-of-coverage

Insert size: 168527; 6.2% error; agarose-gel

Quality coverage: 9.98x in 920 bases; sum-of-coverage

Quality coverage: 10.08x in 920 bases; agarose-gel

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 35571: contig of 35571 bp in length

35572 35671: gap of 100 bp

35672 118670: contig of 82999 bp in length

118671 118770: gap of 100 bp

118771 127664: contig of 8894 bp in length

127665 127764: gap of 100 bp

127765 168018: contig of 40254 bp in length.

Location/Qualifiers

1. 168018

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/clone="RP11-136A14"

/clone_lib="RPC1-11.1"

misc_feature 1. 35571

/note="assembly_fragment:02171
clone_end:SP6
vector_side:left"

misc_feature 35672..118670

misc_feature /note="assembly_fragment:01841
fragment_chain:1"

misc_feature 118771..127664

misc_feature /note="assembly_fragment:02748
fragment_chain:1"

misc_feature 127765..168018

misc_feature /note="assembly_fragment:03955
clone_end:T7
vector_side:right"

BASE COUNT 48201 a 35350 c 36487 g 47678 t 302 others

ORIGIN

Query Match 9.1%; Score 49.4; DB 2; Length 168018;

Best Local Similarity 72.9%; Pred. No. 0.0002;

Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 ACACATGCTTTATTAAAGCATGTATGCCCATCATACCAAGCAAGGATTCTACATG 60

Db 73935 ACACATGCTTTATTAAAGCATGTATGCCCATCATACCAAGGATTCTACATG 73879

QY 61 GTAAGCGCTTCCTATGCGCAAGAGAAACAGACAGCATGAGTGTG 107

Db 73878 GGTAAACCTTCCTATGCGCAAGAGAAACAGACAGCATGAGTGTG 73832

RESULT 13

AC013703/c 176704 bp DNA linear HTG 28-JUN-2000

LOCUS Homo sapiens clone RP11-22F13, WORKING DRAFT SEQUENCE, 8 unordered

DEFINITION pieces.

ACCESSION AC013703

VERSION AC013703.4 GI:8781844

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 176704)

REFERENCE Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome

AUTHORS Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL On Jun 28, 2000 this sequence version replaced gi:7239580.

Unpublished All repeats were identified using RepeatMasker:

2 (bases 1 to 176704)

Unpublished http://ftp.genome.washington.edu/RM/RepeatMasker.html

2 (bases 1 to 176704)

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

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Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

Unpublished

QY 1 ACACAATGGTTATTTAAGGATGTATGCCCCACATCAACCAAGCAGGATTTCTACATG 60

```

Db      1  |||||||||||||||||||||||||||||||||||  |||||
          ACACAAATGTTATTAAGAATGTATGCCACATCAACCTANCAAG---ATTCTACT 57
QY      61  GTAAAGCCTTCCATGTGCGCAAGAGAGAACAACAGACATGAGTTG 107
          |||||||||||||||  |||  ||  ||  |||  |
Db      58  GGTAAACCTTCCTATGCGCAAGAAAAACAACAGCAGGAGTTGAGTTG 104
          |||||||||||||||  |||  ||  ||  |||  |

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Search completed: March 21, 2003, 16:00:15
 Job time : 3803.69 secs

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 11:28:30 ; Search time 393.691 Seconds
(without alignments)
311.799 Million cell updates/sec

Title: US-09-823-101-10

Sequence: 1 acacaatggttattaag.....tcctt~~a~~acagtgacatagca 544

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%

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Database : N_Geneseq_101002.*
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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	54.4	100.0	544	22	AAH43644	SSG #10, Homo sapi
c	2	53.6	9.9	537	24	ABO58989	Human colon cancer
c	3	50.6	9.3	473	24	ABO58742	Human colon cancer
c	4	49.8	9.2	585	24	ABO5588	Human colon cancer
c	5	49.4	9.1	360	24	ABL36725	Human colon tumour
c	6	49.4	9.1	377	24	ABL36425	Human colon tumour
c	7	49.4	9.1	408	23	ABV35049	Human prostate exp
c	8	49.4	9.1	410	24	ABK54824	Human prostate exp
c	9	49.4	9.1	415	23	ABV13979	Human prostate exp

ALIGNMENTS

	RESULT 1
AAH43644	
ID	AAH43644 standard; cDNA; 544 BP.
XX	
AC	AAH43644;
XX	
DT	21-JAN-2002 (first entry)
XX	
DE	SSG #10.
XX	
KW	Stomach cancer specific gene; SSG: polymerase chain reaction; PCR;
KW	amplify; primer: subtracted library; expressed sequence tag; EST; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200175169-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001MO-US10591.
XX	
PR	30-MAR-2000; 2000US-193095P.
XX	
PA	(DIAD-) DIADEXUS INC.
XX	
PI	Pluta J, Chen S, Hu P, Recipon H, Macina RA;
XX	
DR	WPI; 2001-656992/75.
XX	
PT	New Stomach Cancer Specific Genes, useful for diagnosing, monitoring,
PT	staging, imaging or treating cancer, particularly stomach cancer
XX	

PS Claim 1: Page 68-69; 71pp; English.

XX The sequences given in AAH43636-47 represent Stomach Cancer Specific
CC genes (SSG's). These polynucleotides were isolated using a PCR based
CC subtractive hybridisation method on subtracted libraries which were
CC generated for stomach. The cDNA libraries contained expressed sequence
CC tags (EST's) from genes that are stomach cancer specific or are
CC upregulated in stomach. These polynucleotides and the corresponding
CC encoded polypeptides are useful for diagnosing, monitoring, staging,
CC imaging or treating cancer, particularly stomach cancer.

XX Sequence 544 BP: 150 A; 134 C; 142 G; 118 T; 0 other;

Query Match 100.0%; Score 544; DB 22; Length 544;
Best Local Similarity 100.0%; Pred. No. 4,4e-169;

Matches 544; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACATGTTTATTAAGAAATGTATGCCCCACATCACCACCAAGGATCTCATG 60
DB 1 ACACAAATGGTTTATTAAGAAATGTATGCCCCACATCACCACCAAGGATCTCATG 60
OY 61 GTAAAGCCTTCTATGTCACAGAGAAACAGACATGAGTGGAGCTGCTAAGT 120
DB 61 GTAAAGCCTTCTATGTCACAGAGAAACAGACATGAGTGGAGCTGCTAAGT 120
OY 121 GGTGGGTGTCACAGAGATGAGAGAAAGGCGATGAAGGGTGTAGAACATGAATGG 180
DB 121 GGTGGGTGTCACAGAGATGAGAGAAAGGCGATGAAGGGTGTAGAACATGAATGG 180
OY 181 GGGTCTAAGAAATGCTTGATGTAGATTCATGACATAGCGTGTATCTCGGTGAGAC 240
DB 181 GGGTCTAAGAAATGCTTGATGTAGATTCATGACATAGCGTGTATCTCGGTGAGAC 240
OY 241 AATTGCTTATCCGCGTCACACATTCACAGCAGCAATCTGATGCAATCCAGTGCAG 300
DB 241 AATTGCTTATCCGCGTCACACATTCACAGCAGCAATCTGATGCAATCCAGTGCAG 300
OY 301 CTGGATACGACAGCAGCAATCAGAGCTGGCTGCTCTCTTATGAGACAGACCTATC 360
DB 301 CTGGATACGACAGCAGCAATCAGAGCTGGCTGCTCTCTTATGAGACAGACCTATC 360
OY 361 AGCGGTACCGTGTGCTGGTCTGTCAGCAGCAATTCGACAGGCTACTTATGTAACAC 420
DB 361 AGCGGTACCGTGTGCTGGTCTGTCAGCAGCAATTCGACAGGCTACTTATGTAACAC 420
OY 421 ACGGCCAGCTGATTTATCAGAGACTCAACCCAGGCCAAAACCTTACCTTATCTAATAG 480
DB 421 ACGGCCAGCTGATTTATCAGAGACTCAACCCAGGCCAAAACCTTACCTTATCTAATAG 480
OY 481 ACGGCCAGCTTGTGACAGAGATCGCTCTGACAGCTCCCTTAACAGTGCAT 540
DB 481 ACGGCCAGCTTGTGACAGAGATCGCTCTGACAGCTCCCTTAACAGTGCAT 540
OY 541 AGCA 544
DB 541 AGCA 544

RESULT 2
AB059889/c
ID AB059889 standard; cDNA: 537 BP.

XX AB059889;

DT 02-AUG-2002 (first entry)

XX Human colon cancer related nucleotide sequence SEQ ID NO:3584.

KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
XX genetic analysis; diagnostic; antisense therapy; gene; ss.

OS Homo sapiens.
XX

PN WO200229086-A2.

XX 11-APR-2002.

XX 02-OCT-2001: 2001WO-US30732.

XX 02-OCT-2000: 2000US-237271P.

XX (FAR) BAYER CORP.

PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwyer P, Molino GA;
PI Thilagalingam A, Lewis ME;

DR WPI: 2002-42615/45.

PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell
PT or tissue type, and in antisense therapy

PS Claim 1: Fig 1: 796pp; English.

XX AB056306 to AB060787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists.

SQ Sequence 537 BP: 128 A; 155 C; 103 G; 150 T; 1 other;

Query Match 9.9%; Score 53.6; DB 24; Length 537;
Best Local Similarity 60.9%; Pred. No. 3.2e-07;

Matches 103; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

OY 1 ACACATGTTTATTAAGAAATGTATGCCCCACATCAACCAAGGATCTCATG 60
DB 537 ACCAAATGGTTTATTAAGAAATGTATGCCCCACATCAACCAAGGATCTCATG 60
OY 61 GTAAAGCCTTCTATGTCACAGAGAAACAGACATGAGTGGAGCTGCTAAGT 120
DB 61 GTAAAGCCTTCTATGTCACAGAGAAACAGACATGAGTGGAGCTGCTAAGT 120
OY 478 GTAAAGCCTTCTATGTCACAGAGAAACAGACATGAGTGGAGCTGCTAAGT 419
DB 478 GTAAAGCCTTCTATGTCACAGAGAAACAGACATGAGTGGAGCTGCTAAGT 419
OY 121 GGTGGGTGTCACAGAGATGAGAGAAAGGCGATGAAGGGTGTAGAACATGAAGGCGCTAGAA 169
DB 418 AGCAATGAGAGAGAGGCGAGAAAGGCTGTAGAACATGAAGGCGCTAGAA 370

RESULT 3
AB059742/c
ID AB059742 standard; cDNA: 473 BP.

XX AB059742;

DT 02-AUG-2002 (first entry)

XX Human colon cancer related nucleotide sequence SEQ ID NO:3437.

KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
XX genetic analysis; diagnostic; antisense therapy; gene; ss.

OS Homo sapiens.
XX
PN WO200229086-A2.


```
XX 11-APR-2002.
PD 02-OCT-2001; 2001MO-US30732.
XX 02-OCT-2001; 2001MO-US30732.
XX 02-OCT-2000; 2000US-237271P.
XX (FARB ) BAYER CORP.
XX Burgess C, Astle JH, Carroll E, Catino TJ, Divedi P, Molino GA,
PI Thiaulingam A, Lewis ME;
XX WPI; 2002-426115/45.
XX
XX New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell
PT or tissue type, and in antisense therapy -
XX
XX Claim 1; Fig 1; 796pp; English.
XX
XX AB056306 to AB060787 represent isolated nucleic acids (I) differentially
XX expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
XX encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be
XX used in antisense therapy. An antibody immunoreactive with a polypeptide
XX encoded by (I) is useful for detecting cancer in a patient sample, and
XX for detecting the presence or absence of a polynucleotide encoded by a
XX nucleic acid which hybridises to (I) in a cell. A probe/primer derived
XX from (I) can be used for determining the presence of a nucleic acid which
XX hybridises to (I), and for determining the phenotype of cells in a sample
XX of cells from a patient. (I) is useful for determining the presence of
XX colon cancer in a cell or tissue type, for determining the presence or
XX state of other type of cancer, in antisense therapy, to generate
XX microarrays on a solid surface, to identify a chromosome on which the
XX corresponding gene resides, and in tissue profiling, forensics, genetic
XX analysis, mapping and diagnostic applications. (I) can be used to raise
XX antibodies, and to screen for peptide analogues and antagonists.
XX
XX Sequence 473 BP; 112 A; 132 C; 98 G; 131 T; 0 other;
SQ
XX
XX Query Match 9.3%; Score 50.6; DB 24; Length 473;
XX Best Local Similarity 60.4%; Pred. No. 2.9e-06;
XX Matches 102; Conservative 0; Mismatches 64; Indels 3; Gaps 1;
XX
XX 1 ACACAAATGTTTATTAAAGAAATGATGCCCCACATCAACCAAGGATTTCTACATG 60
DB 470 ACACAAATGTTTATTAAAGAAATGATGCCCCACATCAACCTACCAAG--ATTCTACT 414
XX
XX 61 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGCTTGACGTGGCTAGGT 120
DB 413 GGTAAACCTTCTATGTGCCAAGAGAAACAGACATGAGCTTGACGTGGCTAGGT 354
XX
XX 121 GGTGGTGTGCACGCGCAGATGAGAGAGAGGCGCATGGAAGGCTCTAGAA 169
DB 353 CAGGCAATGGAGAGAGCGAGAGAGGCTGAGAACTGAAGGGGGCTAGAA 305
XX
XX
XX RESULT 4
XX ABO59588/c
XX ID ABO59588 standard; cDNA: 585 BP.
XX
XX ABO59588;
XX
XX 02-AUG-2002 (first entry)
XX
XX Human colon cancer related nucleotide sequence SEQ ID NO:3283.
XX
XX Human; colon cancer; cancer; tissue profiling; forensic; mapping;
XX genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200229086-A2.
XX
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PD 11-APR-2002.
XX 02-OCT-2001; 2001MO-US30732.
XX 02-OCT-2001; 2001MO-US30732.
XX 02-OCT-2000; 2000US-237271P.
XX (FARB ) BAYER CORP.
XX Burgess C, Astle JH, Carroll E, Catino TJ, Divedi P, Molino GA,
PI Thiaulingam A, Lewis ME;
XX WPI; 2002-426115/45.
XX
XX New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell
PT or tissue type, and in antisense therapy -
XX
XX Claim 1; Fig 1; 796pp; English.
XX
XX AB056306 to AB060787 represent isolated nucleic acids (I) differentially
XX expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
XX encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be
XX used in antisense therapy. An antibody immunoreactive with a polypeptide
XX encoded by (I) is useful for detecting cancer in a patient sample, and
XX for detecting the presence or absence of a polynucleotide encoded by a
XX nucleic acid which hybridises to (I) in a cell. A probe/primer derived
XX from (I) can be used for determining the presence of a nucleic acid which
XX hybridises to (I), and for determining the phenotype of cells in a sample
XX of cells from a patient. (I) is useful for determining the presence of
XX colon cancer in a cell or tissue type, for determining the presence or
XX state of other type of cancer, in antisense therapy, to generate
XX microarrays on a solid surface, to identify a chromosome on which the
XX corresponding gene resides, and in tissue profiling, forensics, genetic
XX analysis, mapping and diagnostic applications. (I) can be used to raise
XX antibodies, and to screen for peptide analogues and antagonists.
XX
XX Sequence 585 BP; 140 A; 166 C; 118 G; 157 T; 4 other;
SQ
XX
XX Query Match 9.2%; Score 49.8; DB 24; Length 585;
XX Best Local Similarity 59.8%; Pred. No. 6e-06;
XX Matches 101; Conservative 0; Mismatches 67; Indels 1; Gaps 1;
XX
XX 1 ACACAAATGTTTATTAAAGAAATGATGCCCCACATCAACCAAGGATTTCTACATG 60
DB 541 ACCCAATGTTTATTAAAGAAATGATGCCCCACATCAACCTACCAAG--GATTCTTACTG 483
XX
XX 61 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGCTTGACGTGGCTAGGT 120
DB 482 GGTAAACCTTCTATGTGCCAAGAGAAACAGACATGAGCTTGACGTGGCTAGGT 423
XX
XX 121 GGTGGTGTGCACGCGCAGATGAGAGAGAGGCGCATGGAAGGCTCTAGAA 169
DB 422 AGGCAATGGAGAGAGCGAGAGAGGCTGAGAACTGAAGGGGGCTAGAA 374
XX
XX
XX RESULT 5
XX ABL36725
XX ID ABL36725 standard; cDNA: 360 BP.
XX
XX ABL36725;
XX
XX 08-APR-2002 (first entry)
XX
XX Human colon tumour antigen polynucleotide SEQ ID NO:314.
XX
XX Human; colon cancer; colon tumour antigen; cytostatic; vaccine;
XX colon tumour metastatic antigen; diagnosis; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200196388-A2.
XX
XX 20-DEC-2001.
XX
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XX 08-JUN-2001: 2001WO-US18557.
 PF 09-JUN-2000: 2000US-210899P.
 PR 20-FEB-2001: 2001US-270216P.
 XX
 PA (CORI-) CORIXA CORP.
 PI Jiang Y, Harlocker SL, Secretist H;
 XX
 DR WPI: 2002-114514/15.
 XX
 PT Novel isolated colon tumor polynucleotide differentially expressed in
 PI colon tumor or colon metastatic tumor and polypeptides encoded by them,
 CC useful for inhibiting development of cancer in patient -
 XX
 PS Claim 1: SEQ ID 314; 105pp; English.
 XX
 CC ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)
 CC which were isolated from human colon tumour and colon metastatic tumour
 CC cDNA libraries. (I) have cytosolic activity and can be used in vaccine
 CC production. (I) can be used for stimulating and/or expanding T cells
 CC specific for a tumour protein on contact with the T cells. They are also
 CC useful for inhibiting the development of cancer in a patient. (I) can be
 CC used as probes or primers for nucleic acid hybridisation, for preparing
 CC mutant species primers, or primers for use in genetic constructions. (I)
 CC can be used in the diagnosis of a colon tumour.
 XX
 SQ Sequence 360 BP; 104 A; 67 C; 108 G; 79 T; 2 other:
 XX
 Query Match 9.1%; Score 49.4; DB 24; Length 360;
 Best Local Similarity 72.9%; Pred. No. 6.4e-06;
 Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
 OY 1 ACACATGCTTTATTAAAGATGTATGCCCCCATCAACCAAGGATTTCTACAG 60
 DB 1 ACACATGCTTTATTAAAGATGTATGCCCCCATCAACCTAGCAAG--ATTCTACT 57
 OY 61 GTAAGCCTTCTATGTGCCAAGAGAGAAACAGACATGGAGTTG 107
 DB 58 GGTAAACCTTCTATGTGCCAAGAGAGAAACAGACAGAGTTGAGTGG 104
 XX
 RESULT 6
 ABL36425
 ID ABL36425 standard; cDNA: 377 BP.
 XX
 AC ABL36425;
 XX
 DT 08-APR-2002 (first entry)
 XX
 DE Human colon tumour antigen polynucleotide SEQ ID NO:14.
 XX
 KW Human; colon cancer; colon tumour antigen; cytosolic; vaccine;
 KW colon tumour metastatic antigen; diagnosis; gene; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200196388-A2.
 PN
 XX
 PD 20-DEC-2001.
 PD
 XX
 PF 08-JUN-2001: 2001WO-US18557.
 PF
 XX
 PR 09-JUN-2000: 2000US-210899P.
 PR
 XX
 PR 20-FEB-2001: 2001US-270216P.
 PR
 XX
 PA (CORI-) CORIXA CORP.
 PA
 XX
 PI Jiang Y, Harlocker SL, Secretist H;
 PI
 XX
 DR WPI: 2002-114514/15.
 DR
 XX

PT Novel isolated colon tumor polynucleotide differentially expressed in
 PI colon tumor or colon metastatic tumor and polypeptides encoded by them,
 CC useful for inhibiting development of cancer in patient -
 XX
 PS Claim 1: SEQ ID 14; 105pp; English.
 XX
 CC ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)
 CC which were isolated from human colon tumour and colon metastatic tumour
 CC cDNA libraries. (I) have cytosolic activity and can be used in vaccine
 CC production. (I) can be used for stimulating and/or expanding T cells
 CC specific for a tumour protein on contact with the T cells. They are also
 CC useful for inhibiting the development of cancer in a patient. (I) can be
 CC used as probes or primers for nucleic acid hybridisation, for preparing
 CC mutant species primers, or primers for use in genetic constructions. (I)
 CC can be used in the diagnosis of a colon tumour.
 XX
 SQ Sequence 377 BP; 109 A; 71 C; 110 G; 85 T; 2 other:
 XX
 Query Match 9.1%; Score 49.4; DB 24; Length 377;
 Best Local Similarity 72.9%; Pred. No. 6.5e-06;
 Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
 OY 1 ACACATGCTTTATTAAAGATGTATGCCCCCATCAACCAAGGATTTCTACAG 60
 DB 1 ACACATGCTTTATTAAAGATGTATGCCCCCATCAACCTAGCAAG--ATTCTACT 57
 OY 61 GTAAGCCTTCTATGTGCCAAGAGAGAAACAGACATGGAGTTG 107
 DB 58 GGTAAACCTTCTATGTGCCAAGAGAGAAACAGACAGAGTTGAGTGG 104
 XX
 RESULT 7
 ABV35049
 ID ABV35049 standard; cDNA: 408 BP.
 XX
 AC ABV35049;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 35040.
 XX
 KW Human; prostate cancer; cytosolic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200160860-A2.
 PN
 XX
 PD 23-AUG-2001.
 PD
 XX
 PF 20-FEB-2001: 2001WO-US05171.
 PF
 XX
 PR 17-FEB-2000: 2000US-183319P.
 PR
 XX
 PR 16-MAR-2000: 2000US-189862P.
 PR
 XX
 PR 25-MAY-2000: 2000US-207454P.
 PR
 XX
 PR 09-JUN-2000: 2000US-211314P.
 PR
 XX
 PR 18-JUL-2000: 2000US-219007P.
 PR
 XX
 PR 13-DEC-2000: 2000US-255281P.
 PR
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 PI
 XX
 DR WPI: 2001-662795/76.
 DR
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1: Page 7320; 11750pp; English.
 PS
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC	and an antigen-presenting cell expressing (II) is useful for inhibiting
CC	development of cancer in a patient. (I) is useful in the design and
CC	preparation of ribozyme molecules for inhibiting expression of tumour
CC	polypeptides and (I). ABK54531-ABK55464 represent human colon cancer CDNA
CC	sequences of the invention.
XX	
SO	Sequence 410 BP; 109 A; 78 C; 110 G; 106 T; 7 other;
	Query Match 9.1%; Score 49.4; DB 24; Length 410;
	Best Local Similarity 72.9%; Pred. No. 6.8e-06;
	Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
OY	
	1 ACACAGTGGTTATTAAAGGAATGATGGCCACATCAACCAAGCAGGATTCATG 60
Db	31 ACACATATGTTATTATAAGCAATGATGGCCACATCAACCTGACCAAG--ATTCTACT 87
OY	61 GTAAAGCCTTCCTATGTCGCAAGAGAGAAAACAGAGCATGAGTTG 107
Db	88 GGTAAACCTTCCTATGCGCAAGAGAAAACAGAGCATGAGTTGAGTGG 134
RESULT 9	
ABV13979	
ID	ABV13979 standard; CDNA: 415 BP.
XX	
AC	ABV13979;
XX	
DT	13-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker CDNA 13970.
XX	
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW	pharmacogenomic marker; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200160860-A2.
XX	
PD	23-AUG-2001.
XX	
PF	20-FEB-2001; 2001WO-US05171.
XX	
PR	17-FEB-2000; 2000US-183319P.
XX	
PR	16-MAR-2000; 2000US-189862P.
XX	
PR	25-MAY-2000; 2000US-207454P.
XX	
PR	09-JUN-2000; 2000US-211314P.
XX	
PR	18-JUL-2000; 2000US-219007P.
XX	
PR	13-DEC-2000; 2000US-255281P.
XX	
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	
PI	Schlegel R, Endege WO, Monahan JE;
XX	
DR	WPI: 2001-662795/76.
XX	
PT	Novel isolated nucleic acid molecule associated with cancerous state of
PT	prostate cells and correlating with presence of prostate cancer, useful
PT	for detecting presence of prostate cancer, stage of prostate cancer
XX	
PS	Claim 1; Page 2330; 11750pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC	specification or its complement. (I) is useful for:
CC	(a) assessing whether a patient is afflicted with prostate cancer;
CC	(b) monitoring the progression of prostate cancer in a patient;
CC	(c) assessing the efficacy of a test compound to inhibit prostate
CC	cancer in a patient;
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC	in a patient;
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;
CC	(f) assessing the prostate cell carcinogenic potential of a compound;
CC	(g) determining whether prostate cancer has metastasized in a patient;
CC	(h) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 415 BP; 118 A; 82 C; 122 G; 93 T; 0 other;
Query Match 9.1%; Score 49.4; DB 23; Length 415;
Best Local Similarity 72.9%; Pred. No. 6.9e-06;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
OY 1 ACACATGCTTTTAAAGAAATGTATGGCCCATCATCAACCAAGAGGATTTCTACATG 60
DB 11 ACACATGCTTTTAAAGAAATGTATGGCCCATCATCAACCTAGCAAG---ATTCTACT 67
OY 61 GTAAGCCTTCTATGTGCCAAGAGAAACAGAGCATGAGTTG 107
DB 68 GGTAAACCTTCTATGTGCCAAGAGAAACAGAGCATGAGTTG 114
RESULT 10
ABV13939
ID ABV13939 standard; cDNA; 418 BP.
XX
AC ABV13939;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 13930.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
XX
PR 16-MAR-2000; 2000US-189862P.
XX
PR 25-MAY-2000; 2000US-207454P.
XX
PR 09-JUN-2000; 2000US-211314P.
XX
PR 18-JUL-2000; 2000US-219007P.
XX
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 2322; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 418 BP; 123 A; 76 C; 112 G; 107 T; 0 other;
Query Match 9.1%; Score 49.4; DB 23; Length 418;
Best Local Similarity 72.9%; Pred. No. 6.9e-06;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
OY 1 ACACATGCTTTTAAAGAAATGTATGGCCCATCATCAACCAAGAGGATTTCTACATG 60
DB 5 ACACATGCTTTTAAAGAAATGTATGGCCCATCATCAACCTAGCAAG---ATTCTACT 61
OY 61 GTAAGCCTTCTATGTGCCAAGAGAAACAGAGCATGAGTTG 107
DB 62 GGTAAACCTTCTATGTGCCAAGAGTAAACAGAGCATGAGTTG 108
RESULT 11
ABV35087
ID ABV35087 standard; cDNA; 457 BP.
XX
AC ABV35087;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 35078.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
XX
PR 16-MAR-2000; 2000US-189862P.
XX
PR 25-MAY-2000; 2000US-207454P.
XX
PR 09-JUN-2000; 2000US-211314P.
XX
PR 18-JUL-2000; 2000US-219007P.
XX
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 7326; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

SQ Sequence 457 BP; 126 A; 96 C; 135 G; 100 T; 0 other;

Query Match 9.1%; Score 49.4; DB 23; Length 457;

Best Local Similarity 72.9%; Pred. No. 7.2e-06;

Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

```
OY 1 ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCAAGCAAGGATTTCTACATG 60
    |||||||
DB 57 ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCTAGCAAG---ATTCTACT 113
    |||||||
OY 61 GTAAGCCTTCCCTATGTGCCAAGAGAAGAACAGACATGAGTTG 107
    |||||||
DB 114 GGTAAACCTTCCCTATGTGCCAAGAAAACAAACAGAGAGTTGAGTGG 160
    |||||||
```

RESULT 12

ID ABV04810 standard; cDNA; 466 BP.

XX ABV04810;

DT 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 4801.

XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN WO200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

DR WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -

PS Claim 1; Page 826; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 466 BP; 131 A; 96 C; 136 G; 99 T; 4 other;

Query Match 9.1%; Score 49.4; DB 23; Length 466;

Best Local Similarity 72.9%; Pred. No. 7.2e-06;

Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

```
OY 1 ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCAAGCAAGGATTTCTACATG 60
    |||||||
DB 27 ACACAAATGGTTTATTAAAGAAATGTATGGCCACATCAACCTAGCAAG---ATTCTACT 83
    |||||||
OY 61 GTAAGCCTTCCCTATGTGCCAAGAGAAGAACAGACATGAGTTG 107
    |||||||
DB 84 GGTAAACCTTCCCTATGTGCCAAGAAAACAAACAGAGAGTTGAGTGG 130
    |||||||
```

RESULT 13

ID ABV43896 standard; cDNA; 529 BP.

XX ABV43896;

DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 43887.

XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN WO200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

DR WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -

PS Claim 1; Page 8730; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 529 BP; 148 A; 106 C; 152 G; 123 T; 0 other;

Query Match 9.1%; Score 49.4; DB 23; Length 529;

Best Local Similarity 72.9%; Pred. No. 7.7e-06;

Query Match	9.18;	Score	49.4;	DB	23,	Length	529;
Best Local Similarity	72.98;	Pred. NO.	7.7e-06;				
Matches	78;	Conservative	0;	Mismatches	26;	Indels	3;
						Gaps	1.

Search completed: March 21, 2003, 11:54:22
Job time : 399.891 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 16:26:05 ; Search time 61.3611 Seconds
(without alignments)
2718.857 Million cell updates/sec

Title: US-09-823-101-10

Perfect score: 544
Sequence: 1 acacaatggttataaag.....tcttaacagtgacataagca 544

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/6CTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	49.4	9.1	1114	2	US-08-468-413-1
C 2	49.4	9.1	1114	3	US-09-162-508-1
C 3	49.4	9.1	1114	5	PCR-US95-07169-1
C 4	42.4	7.8	7218	1	US-08-232-463-14
C 5	33	6.1	741	4	US-09-328-111-670
C 6	32.8	6.0	1215	4	US-09-556-877-61
C 7	32.8	6.0	1215	4	US-09-620-412C-61
C 8	32.8	6.0	2826	3	US-09-010-998-1
C 9	31	5.7	81001	4	US-09-750-580-1
C 10	30.2	5.6	289	4	US-09-007-005-17
C 11	30.2	5.6	289	4	US-09-244-796-17
C 12	30.2	5.6	16389	4	US-09-741-154-3
C 13	30	5.5	49272	4	US-08-614-770A-1
C 14	29.6	5.4	703	2	US-09-328-111-262
C 15	28.6	5.3	880	4	US-08-668-255-4
C 16	28.4	5.2	1699	2	US-09-171-209-15
C 17	28.4	5.2	1699	2	US-08-484-993B-3
C 18	28.4	5.2	1699	2	US-08-484-158B-3
C 19	28.4	5.2	1699	2	US-08-484-596A-3
C 20	28.4	5.2	1699	2	US-08-480-150A-3
C 21	28.4	5.2	1699	2	US-08-458-731-3
C 22	28.4	5.2	1699	2	US-08-149-223A-3
C 23	28.4	5.2	4977	1	US-08-030-096-7
C 24	28.4	5.2	1296	5	PCR-US94-12912-3
C 25	28.2	5.1	546	4	US-09-697-367-11
C 26	28	5.1	168575	4	US-09-426-290-1
C 27	28	5.1	168575	4	US-09-426-290-1

C 28	27.8	5.1	1182	4	US-09-221-017B-1039	Sequence 1039, Ap
C 29	27.6	5.1	278	1	US-08-178-477B-33	Sequence 33, Appl
C 30	27.6	5.1	4603	1	US-08-258-261B-17	Sequence 17, Appl
C 31	27.6	5.1	4603	1	US-08-456-837-17	Sequence 17, Appl
C 32	27.6	5.1	4603	1	US-08-457-342-17	Sequence 17, Appl
C 33	27.6	5.1	4603	1	US-08-457-646A-17	Sequence 17, Appl
C 34	27.6	5.1	4603	1	US-08-458-076A-17	Sequence 17, Appl
C 35	27.6	5.1	4603	1	US-08-457-335A-17	Sequence 17, Appl
C 36	27.6	5.1	4603	1	US-08-729-214-17	Sequence 17, Appl
C 37	27.6	5.1	4603	3	US-09-028-934-17	Sequence 11, Appl
C 38	27.6	5.1	5698	1	US-08-761-258-11	Sequence 11, Appl
C 39	27.6	5.1	5698	2	US-08-977-306-11	Sequence 11, Appl
C 40	27.4	5.0	248	4	US-09-007-005-32	Sequence 32, Appl
C 41	27.4	5.0	248	4	US-09-244-796-32	Sequence 32, Appl
C 42	27.4	5.0	277	4	US-09-007-005-3	Sequence 3, Appl
C 43	27.4	5.0	277	4	US-09-244-796-3	Sequence 3, Appl
C 44	27.4	5.0	668	1	US-08-259-745A-13	Sequence 13, Appl
C 45	27.4	5.0	2694	1	US-08-147-890-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-468-413-1/c
; Sequence 1, Application US/08468413
; Patent No. 5861494
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Colon Specific Gene
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,413
; FILING DATE: 06 JUN 95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1114 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; US-08-468-413-1

Query Match 9.1%; Score 49.4; DB 2; Length 1114;
Best Local Similarity 72.9%; Pred. No. 2.3e-07;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

1 ACACAATGCTTATTAAAGATGTATGCGCCACATCAACCAAGCAAGCATCTACATG 60
|||||

Db 1112 ACACATGGTTATTAAAGAAATGTATGCCACATCAACTAGCAAG---ATTCTACT 1056
QY 61 GTAAGCCTTCTATGTGCCAGAGAAACAAGACGATGAGTTG 107
1 ||||||||||| ||| ||| ||| ||| |||
Db 1055 GGTAACCTTCTATGCGCAAGAAACAAAGACGAGCTTGAATGG 1009

RESULT 2
US-09-162-508-1/C

; Sequence 1, Application US/09162508
; Patent No. 6080722
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Colon Specific Gene
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/162,508
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,413
; FILING DATE: 06 JUN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1114 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; US-09-162-508-1

Query Match 9.1%; Score 49.4; DB 3; Length 1114;
Best Local Similarity 72.9%; Pred. No. 2.3e-07;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 ACACATGGTTATTAAAGAAATGTATGCCACATCAACTAGCAAGGATTCATCAGT 60
|||||
Db 1112 ACACATGGTTATTAAAGAAATGTATGCCACATCAACTAGCAAG---ATTCTACT 1056
|||||
QY 61 GTAAGCCTTCTATGTGCCAGAGAAACAAGACGATGAGTTG 107
1 ||||||||||| ||| ||| ||| ||| |||
Db 1055 GGTAACCTTCTATGCGCAAGAAACAAAGACGAGCTTGAATGG 1009

RESULT 3

PCT-US95-07169-1/C
; Sequence 1, Application PC/TUS9507169
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Colon Specific Gene
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07169
; FILING DATE: 06 JUN 95
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1114 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; PCT-US95-07169-1

Query Match 9.1%; Score 49.4; DB 5; Length 1114;
Best Local Similarity 72.9%; Pred. No. 2.3e-07;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 ACACATGGTTATTAAAGAAATGTATGCCACATCAACTAGCAAGGATTCATCAGT 60
|||||
Db 1112 ACACATGGTTATTAAAGAAATGTATGCCACATCAACTAGCAAG---ATTCTACT 1056
|||||
QY 61 GTAAGCCTTCTATGTGCCAGAGAAACAAGACGATGAGTTG 107
1 ||||||||||| ||| ||| ||| ||| |||
Db 1055 GGTAACCTTCTATGCGCAAGAAACAAAGACGAGCTTGAATGG 1009

RESULT 4

US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435


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CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 670
LENGTH: 741
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(741)
OTHER INFORMATION: n = A,T,C or G
US-09-328-111-670

Query Match
Best Local Similarity 6.1%; Score 33; DB 4; Length 741;
Matches 48; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 211 GGTACACATGAGGTATCTGGGTGTGACATTCGTAAATCCGGCTACACATTCACGC 270
Db 580 GGGCCATAGCTTGCTTCCCTGGGGGGAATTTGTAATCCGGTCCACNAATTTCCCC 639
QY 271 AGCAACATCATCTGATGCC 287
Db 640 ACCAACNTTCCNAAC 656

RESULT 6
US-09-556-877-61
Sequence 61, Application US/09556877
Patent No. 6432916
GENERAL INFORMATION:
APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir
APPLICANT: Filing, Steve
APPLICANT: Malsoneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 61
LENGTH: 1215
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-556-877-61

Query Match
Best Local Similarity 6.0%; Score 32.8; DB 4; Length 1215;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 15 TAAAGATGTATGGCCACATCAACCAAGCAGATTTTCATGCTGAACCTTCTCTA 74
Db 929 TCATCGAATAAATATACCAACCACTGAGCGTTCATGACAGTTGAACCTTCTCTA 988
QY 75 TGTGCCAAGAGAGAGAACAGAGCATGGAGTT 106
Db 989 TTTTCGATTCGATGAACCGTCATCCATTTT 1020

RESULT 7
US-09-620-412C-61
Sequence 61, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7

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CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
SEQ ID NO 61
LENGTH: 1215
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-620-412C-61

Query Match 6.0%; Score 32.8; DB 4; Length 1215;
Best Local Similarity 59.8%; Pred. No. 0.17;

Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 15 TAAAGAAATGTATGGCCCATCAACCAAGGATTTCTACATGCTAAAGCCTTCCTA 74
DB 929 TATCGAATAAATAATAGACCACTCAACACACTAGCCCTTATGATGAGTTCCTTCTTA 988
QY 75 TGTGCCAAGAGAGAAACAGAGCATGAGTT 106
DB 989 TTTTGAATTCATGTAACCGTCATCCATTT 1020

RESULT 8

US-09-010-998-1
Sequence 1, Application US/09010998
Patent No. 6103872

GENERAL INFORMATION:

APPLICANT: Snyder, Solomon
APPLICANT: Jafirey, Samle
APPLICANT: Snowman, Adele
APPLICANT: Eliasson, Mikael
APPLICANT: Cohen, No. 6103872m
TITLE OF INVENTION: CAPON, a protein that binds
TITLE OF INVENTION: neuronal nitric oxide synthase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,998
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107, 73424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2826 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-010-998-1

Query Match 6.0%; Score 32.8; DB 3; Length 2826;

Best Local Similarity 53.0%; Pred. No. 0.28;
Matches 70; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 42 AACCAAGGATTTCTACATGCTAAAGCCTTCTATGTGCCAAGAGAGAAACAGACATG 101
DB 1704 AACCAAGGATTTCTACATGCTAAAGCCTTCTATGTGCCAAGAGAGAAACAGACATG 1763
QY 102 GAGTTGACCGTGTAGGCTGAGTGTGTCACGCGAGATGAGAGAAAGGCGATGAAGG 161
DB 1764 GAGTCAAGCATCGCCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1823

QY 162 TCGTAGAACGCA 173
DB 1824 TGTGCGCAGGAA 1835

RESULT 9

US-09-750-580-1/c
Sequence 1, Application US/09750580
Patent No. 6455280

GENERAL INFORMATION:

APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duchet, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebbels-Reed, Dana
APPLICANT: Sailer-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US2 CIP
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm

SEQ ID NO 1

LENGTH: 81001

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 10946..12946

OTHER INFORMATION: 5' regulatory region

NAME/KEY: exon

LOCATION: 12947..12958

OTHER INFORMATION: exon 1

NAME/KEY: exon

LOCATION: 13470..13526

OTHER INFORMATION: exon 2

NAME/KEY: exon

LOCATION: 13641..13752

OTHER INFORMATION: exon 3

NAME/KEY: exon

LOCATION: 14271..15968

OTHER INFORMATION: exon 4

NAME/KEY: misc_feature

LOCATION: 15969..17969

OTHER INFORMATION: 3' regulatory region

NAME/KEY: allele

LOCATION: 1239

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OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
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NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
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Query Match 5.7%; Score 31; DB 4; Length 81001;
Best Local Similarity 59.8%; Pred. No. 8.2;
Matches 52; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 71 CCTATGTCCCAAGCAGCAACAGCATGAGATTGGACGTGGCTGAGTGGTGTG 130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66840 CCTCTGTCTCAGGTCTCAGCAACCTGTGTGTGACGTGGTGGGTGGTGTG 66781
QY 131 CACGGCAGATGAGAGAAAGGCATGA 157
    ||||| ||| ||| ||| |||
DB 66780 GGAAGCAGAGATGAGGCGACGAAAGA 66754
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RESULT 10
US-09-007-005-17
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
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251 TCCGCGTCACACATTCCAGCAGCAACATAC⁺TGATGCC 287

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QY      206 TTCATGGTACACTAGCGGTATTCCTGGGTGTGACCAATTCGTTAATC 252
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Db      314 AGTAAGGTGGCCATCATGCTTGCCCGTSGCTGACTGTACGCTTTC 360

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Search completed: March 21, 2003, 19:16:59
Job time : 135.361 secs

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GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 23:43:06 ; Search time 116.277 Seconds
(without alignments)
3628.058 Million cell updates/sec

Title: US-09-823-101-10

Perfect score: 544

Sequence: 1 acaaatgttataaag.....tcttaacagtacatagca 544

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 538826 segs, 387737923 residues

Total number of hits satisfying chosen parameters: 1077652

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications -NA:*

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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	49.4	9.1	357	US-10-046-935-314	Sequence 314, App
3	49.4	9.1	357	US-09-878-178-314	Sequence 314, App
4	49.4	9.1	374	US-10-046-935-14	Sequence 14, Appl
5	49.4	9.1	374	US-09-878-178-14	Sequence 14, Appl
6	49.4	9.1	410	US-09-919-580-294	Sequence 294, App
7	49.4	9.1	541	US-10-046-935-1586	Sequence 1586, App
8	49.4	9.1	541	US-09-878-178-1586	Sequence 1586, App
9	49.4	9.1	1114	US-10-025-380-1071	Sequence 1071, Ap
10	49.4	9.1	1114	US-10-025-380-1074	Sequence 1074, Ap
11	49.4	9.1	1114	US-09-922-217-1071	Sequence 1071, Ap
12	49.4	9.1	1114	US-09-922-217-1074	Sequence 1074, Ap
13	49.4	9.1	1114	US-09-833-263-1071	Sequence 1071, Ap
14	49.4	9.1	1114	US-09-833-263-1074	Sequence 1074, Ap
15	48.4	8.9	473	US-10-046-935-2190	Sequence 2190, Ap
16	48.4	8.9	473	US-09-878-178-2190	Sequence 2190, Ap
17	48.4	8.9	554	US-09-919-580-462	Sequence 462, App
18	48.4	8.9	558	US-09-998-598-2537	Sequence 2537, Ap
19	47.8	8.8	306	US-10-046-935-754	Sequence 754, App

20	47.8	8.8	306	US-09-878-178-754	Sequence 754, App
21	47.8	8.8	463	US-10-046-935-1136	Sequence 1136, Ap
22	47.8	8.8	463	US-09-878-178-1136	Sequence 1136, Ap
23	47.8	8.8	530	US-10-046-935-1204	Sequence 1204, Ap
24	47.8	8.8	530	US-09-878-178-1204	Sequence 1204, Ap
25	47.8	8.8	541	US-10-046-935-307	Sequence 307, App
26	47.8	8.8	541	US-09-878-178-307	Sequence 307, App
27	47.8	8.8	549	US-10-025-380-497	Sequence 497, App
28	47.8	8.8	549	US-09-922-217-497	Sequence 497, App
29	47.8	8.8	549	US-09-833-263-497	Sequence 497, App
30	47.8	8.8	1152	US-10-025-380-1072	Sequence 1072, Ap
31	47.8	8.8	1152	US-09-922-217-1072	Sequence 1072, Ap
32	47.8	8.8	1152	US-09-833-263-1072	Sequence 1072, Ap
33	47.4	8.7	78	US-10-025-380-324	Sequence 324, App
34	47.4	8.7	78	US-09-922-217-324	Sequence 324, App
35	47.4	8.7	78	US-09-833-263-324	Sequence 324, App
36	37.4	6.9	827	US-10-202-193-156	Sequence 156, App
37	37.2	6.8	518	US-10-042-125A-50	Sequence 50, Appl
38	37	6.1	741	US-09-879-536-670	Sequence 670, Appl
39	33	6.1	1215	US-09-841-132-61	Sequence 61, Appl
40	32.8	6.0	1215	US-09-841-132-61	Sequence 430, App
41	32.8	6.0	1398	US-09-764-868-1351	Sequence 1351, Ap
42	31.6	5.8	11881	US-09-764-868-1351	Sequence 1353, Ap
43	31.6	5.8	11881	US-09-764-868-1353	Sequence 2124, Ap
44	31.6	5.8	11881	US-09-764-869-2124	Sequence 106, App
45	31.4	5.8	772	US-10-184-644-106	

ALIGNMENTS

RESULT 1	
US-09-823-101-10	
Sequence 10, Application US/09823101	
Patent No. US20020068307A1	
GENERAL INFORMATION:	
APPLICANT: Pluta, Jason	
APPLICANT: Chen, Sel-Yu	
APPLICANT: Hu, Ping	
APPLICANT: Recipon, Herve	
APPLICANT: Macina, Roberto	
TITLE OF INVENTION: Compositions and Methods for Diagnosing, Monitoring, and Treating Stomach Cancer	
TITLE OF INVENTION: Staging, Imaging, and Treating Stomach Cancer	
FILE REFERENCE: DEX-0205	
CURRENT APPLICATION NUMBER: US/09/823,101	
CURRENT FILING DATE: 2001-03-30	
PRIOR APPLICATION NUMBER: 60/193,095	
PRIOR FILING DATE: 2000-03-30	
NUMBER OF SEQ ID NOS: 19	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 10:	
LENGTH: 544	
TYPE: DNA	
ORGANISM: Homo sapiens	
Query Match	100.0%; Score 544; DB 10; Length 544;
Best Local Similarity	100.0%; Pred. No. 5.8e-171; Indels 0; Gaps 0;
Matches 544; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 1	ACCAATGCTTTTAAAGATGTATGCGCCACATCAACCAAGCAAGGATTTCTACATG 60
DB 1	ACCAATGCTTTTAAAGATGTATGCGCCACATCAACCAAGCAAGGATTTCTACATG 60
QY 61	GTAAGCCTTCTATGTGCCAAGAGAAGACAGACATGAGTTGGACGTGGCTAGGT 120
DB 61	GTAAGCCTTCTATGTGCCAAGAGAAGACAGACATGAGTTGGACGTGGCTAGGT 120
QY 121	GGTGGGTGTCAGGCGAGATGAGAGAGAGGCGATGAGGCTGTAAACGATGAATGG 180
DB 121	GGTGGGTGTCAGGCGAGATGAGAGAGAGGCGATGAGGCTGTAAACGATGAATGG 180
QY 181	GGGTCTAAGATGCTGTGATGATTCATGATACACTACGCTGTATTCCTGGGTGAC 240

Db	181	GGGTCTAGAAATGCTGGATGTAGATTTCATGTACTAGCGTGTATTCTCGGGTGTGAC	240
Oy	241	AATTCGTTAAATCCCGCTTCACACATTCCAGCAGCAACTACTGATGCCAATCCAGTGACAG	300
Db	241	AATTCGTTAAATCCCGCTTCACACATTCCAGCAGCAACTACTGATGCCAATCCAGTGACAG	300
Oy	301	CTCGATTACGCACAGCAGCAATCAGACGACTGGCTGCTCTCCTTTATGACACAGACCTATC	360
Db	301	CTGGATTACGCACAGCAGCAATCAGACGACTGGCTGCTCTCTCTTTATGACACAGACCTATC	360
Oy	361	AGGCGTACCCGTGTGCTTGCGTCTCTGTGTACACGCCAATTCGCACGGCTACTTATGTAAAC	420
Db	361	AGGCGTACCCGTGTGCTTGCGTCTCTGTGTACACGCCAATTCGCACGGCTACTTATGTAAAC	420
Oy	421	ACGGGCGAGCGATTATACAGGAGATCAACCCAGGCGCAAAACCTTACGCTTATCTATTAAG	480
Db	421	ACGGGCGAGCGATTATACAGGAGATCAACCCAGGCGCAAAACCTTACGCTTATCTATTAAG	480
Oy	481	ACGGGCGAGTTTGCACGAGAGATCGCTCTGCACGCTTCACAGACTCTCTTAACAGTGACAT	540
Db	481	ACGGGCGAGTTTGCACGAGAGATCGCTCTGCACGCTTCACAGACTCTCTTAACAGTGACAT	540
Oy	541	AGCA 544	
Db	541	AGCA 544	

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RESULT 2
US-10-046-935-314
Sequence 314, Application US/10046935
Patent No. US20020156011A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secretst, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF COLON CANCER
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 314
LENGTH: 357
TYPE: DNA
ORGANISM: Homo sapiens
US-10-046-935-314

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[illegible]

RESULT 3
 US-09-878-178-314
 Sequence 314, Application US/09878178
 Patent No. US20020177552A1
GENERAL INFORMATION:
 APPLICANT: Jiang, Yugu
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

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? TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
? FILE REFERENCE: 210121.527
? CURRENT APPLICATION NUMBER: US/09/878,178
? CURRENT FILING DATE: 2001-06-08
? NUMBER OF SEQ ID NOS: 2237
? SOFTWARE: FASTSEQ For Windows Version 4.0
? SEQ ID NO: 314
? LENGTH: 357
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-878-178-314

Query Match          9.1%; Score 49.4; DB 9; Length 357;
Best Local Similarity 72.9%; Pred. No. 1.9e-06;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1.

QY 1 ACACATGCTTTATTAAGGAATGTATGCGCCACATCAACCAAGCAAGGATTTCTACATG 60
DB 1 ACACATGCTTTATTAAGGAATGTATGCGCCACATCAACCAAGCAAGGATTTCTACT 57
QY 61 GTAAGGCTTCTCATGTGCGCCAGAGAGAAACAAACAGCATGTGAGTTG 107
DB 58 GGTAACCTTCTCATGTGCGCCAGAGAGAAACAAACAGCATGTGAGTTG 104

```

```

: RESULT 4
: US-10-046-935-14
: Sequence 14, Application US/10046935
: Patent No. US20020156011A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Yugu
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Secrist, Heather
: APPLICANT: Wang, Aijun
: APPLICANT: Stolk, John A
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
: FILE REFERENCE: 210121.527C1
: CURRENT APPLICATION NUMBER: US/10/046,935
: CURRENT FILING DATE: 2002-01-15
: NUMBER OF SEQ ID NOS: 2239
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 374
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-046-935-14

```

	Query Match	9.1%	Score 49.4;	DB 9,	Length 374;
	Best Local Similarity	72.9%;	Pred.	No. 2e-06;	
	Matches	78;	Conservative	0;	Mismatches 26; Indels 3; Gaps 1;
Oy	1 ACACATGCTTATTAAAGGAATFATGGCCCATCAACCAAGCAGGATTTACATG	60			
Db	1 ACACATGCTTATTAAAGGAATFATGGCCCATCAACATGAGAAGS--ATTCTACT	57			
Oy	61 GTAAGCCTTCCTATGTGCACAAGAGAAAACAGACATGGAGTTG	107			
Db	58 GTTAACCTTCCTATGTGCCAAGAAAAACAAGCAGGAGTTGATGG	104			

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RESULT 5
US-09-878-178--14
: Sequence 14: Application US/09678178
: Patent No. US20020177552A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Yugu
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Seelst, Heather
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
: FILE REFERENCE: 210121.527
: CURRENT APPLICATION NUMBER: US/09/878,178

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RESULT 9
US-10-025-380-1071/c
; Sequence 1071, Application US
; Publication No. US20020182191
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J
; APPLICANT: Secrist, Heather

```

: APPLICANT: Benson, Darin R.
: APPLICANT: Meagher, Madeleine Joy
: APPLICANT: Stolk, John A.
: APPLICANT: Wang, Tonglong
: APPLICANT: Jiang, Yugu
: APPLICANT: Smith, Carole L.
: APPLICANT: King, Gordon E.
: APPLICANT: Wang, Aljun
: APPLICANT: Clapper, Jonathan D.
: APPLICANT: Skelky, Yasir A. W.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick Thomas S.
: APPLICANT: Carter, Darick
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.471C14
: CURRENT APPLICATION NUMBER: US/10/025,380
: CURRENT FILING DATE: 2001-12-19
: NUMBER OF SEQ ID NOS: 1129
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1071
: LENGTH: 1114
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-025-380-1071

Query Match          9.1%; Score 49.4; DB 9; Length 1114;
Best Local Similarity 72.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
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Qy 1 ACACATGCTTTATTAAAGAAATGTATGGCCACATCAACCAAGAGGATTTCTACATG 60
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Db 1112 ACACATGCTTTATTAAAGAAATGTATGGCCACATCAACCTGACGAAG---ATTCTACT 1056
    |||||
Qy 61 GTAAACCTTCTTATGTGCCAAGAGCAAGAAACAGACATGGAGTTG 107
    |||||
Db 1055 GGTAAACCTTCTTATGTGCCAAGAGCAAGAAACAGACAGAGTTGAGTGG 1009
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RESULT 10
US-10-025-380-1074/c
: Sequence 1074, Application US/10025380
: Publication No. US20020182191A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Lodes, Michael J.
: APPLICANT: Secrist, Heather
: APPLICANT: Benson, Darin R.
: APPLICANT: Meagher, Madeleine Joy
: APPLICANT: Stolk, John A.
: APPLICANT: Wang, Tonglong
: APPLICANT: Jiang, Yugu
: APPLICANT: Smith, Carole L.
: APPLICANT: King, Gordon E.
: APPLICANT: Wang, Aljun
: APPLICANT: Clapper, Jonathan D.
: APPLICANT: Skelky, Yasir A. W.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick Thomas S.
: APPLICANT: Carter, Darick
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.471C14
: CURRENT APPLICATION NUMBER: US/10/025,380
: CURRENT FILING DATE: 2001-12-19
: NUMBER OF SEQ ID NOS: 1129
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1074
: LENGTH: 1114
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-025-380-1074
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Query Match          9.1%; Score 49.4; DB 9; Length 1114;
Best Local Similarity 72.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

Qy 1 ACACATGCTTTATTAAAGAAATGTATGGCCACATCAACCAAGAGGATTTCTACATG 60
    |||||
Db 1112 ACACATGCTTTATTAAAGAAATGTATGGCCACATCAACCTGACGAAG---ATTCTACT 1056
    |||||
Qy 61 GTAAACCTTCTTATGTGCCAAGAGCAAGAAACAGACATGGAGTTG 107
    |||||
Db 1055 GGTAAACCTTCTTATGTGCCAAGAGCAAGAAACAGACAGAGTTGAGTGG 1009
    |||||
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```

RESULT 11
US-09-922-217-1071/c
: Sequence 1071, Application US/09922217
: Patent No. US2002007641A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Lodes, Michael J.
: APPLICANT: Secrist, Heather
: APPLICANT: Benson, Darin R.
: APPLICANT: Meagher, Madeleine Joy
: APPLICANT: Stolk, John A.
: APPLICANT: Wang, Tonglong
: APPLICANT: Jiang, Yugu
: APPLICANT: Smith, Carole Lynn
: APPLICANT: King, Gordon E.
: APPLICANT: Wang, Aljun
: APPLICANT: Clapper, Jonathan D.
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.471C13
: CURRENT APPLICATION NUMBER: US/09/922,217
: CURRENT FILING DATE: 2001-08-03
: NUMBER OF SEQ ID NOS: 1124
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1071
: LENGTH: 1114
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-922-217-1071

Query Match          9.1%; Score 49.4; DB 10; Length 1114;
Best Local Similarity 72.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
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Qy 1 ACACATGCTTTATTAAAGAAATGTATGGCCACATCAACCAAGAGGATTTCTACATG 60
    |||||
Db 1112 ACACATGCTTTATTAAAGAAATGTATGGCCACATCAACCTGACGAAG---ATTCTACT 1056
    |||||
Qy 61 GTAAACCTTCTTATGTGCCAAGAGCAAGAAACAGACATGGAGTTG 107
    |||||
Db 1055 GGTAAACCTTCTTATGTGCCAAGAGCAAGAAACAGACAGAGTTGAGTGG 1009
    |||||

RESULT 12
US-09-922-217-1074/c
: Sequence 1074, Application US/09922217
: Patent No. US2002007641A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Lodes, Michael J.
: APPLICANT: Secrist, Heather
: APPLICANT: Benson, Darin R.
: APPLICANT: Meagher, Madeleine Joy
: APPLICANT: Stolk, John A.
: APPLICANT: Wang, Tonglong
: APPLICANT: Jiang, Yugu
: APPLICANT: Smith, Carole Lynn
: APPLICANT: King, Gordon E.
: APPLICANT: Wang, Aljun
: APPLICANT: Clapper, Jonathan D.
```

RESULT 14
US-09-833-263-1074/c
Sequence 1074, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeline J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471c12

Search completed: March 22, 2003, 00:21:36
Job time : 119.277 secs

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Copyright (c) 1993 - 2003 CompuGen Ltd.

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Title: US-09-823-101-10

Perfect score: 544

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Scoring table:

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Searched: 16154066 seqs, 8097743376 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	49.4	9.1	162	9	AI444965 t193b01.x
3	49.4	9.1	212	10	AW044042 wv99h11.x
4	49.4	9.1	218	9	AI470732 t116f09.x
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6	49.4	9.1	259	9	AA582738 nm39a03.s

7	49.4	9.1	279	9	AA583270 nm41g03.s
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9	49.4	9.1	283	9	AI537454 tp04a06.x
10	49.4	9.1	286	9	AA581266 nd38e10.s
11	49.4	9.1	293	9	AA837983 oe89a09.s
12	49.4	9.1	297	9	AA586123 nk10g08.s
13	49.4	9.1	321	9	AI933755 wm43e09.x
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15	49.4	9.1	345	9	AA584947 nm41p08.s
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17	49.4	9.1	358	9	AI452604 t127f09.x
18	49.4	9.1	393	9	AI888532 wn21e04.x
19	49.4	9.1	397	9	AA552328 nk04e01.s
20	49.4	9.1	398	9	AA588112 nk10e12.s
21	49.4	9.1	403	9	AA552602 nk12a12.s
22	49.4	9.1	411	9	AA552452 nk12f01.s
23	49.4	9.1	412	9	AA574080 nk11f09.s
24	49.4	9.1	414	9	AA551912 nk13c01.s
25	49.4	9.1	420	9	AA552304 nk06f07.s
26	49.4	9.1	426	9	AA552106 nk05e12.s
27	49.4	9.1	427	9	AA552296 nk06e09.s
28	49.4	9.1	434	9	AA552332 nk04e05.s
29	49.4	9.1	435	9	AI446121 t107b03.x
30	49.4	9.1	439	9	AA573769 nk07d04.s
31	49.4	9.1	439	10	AM130226 xf47d04.x
32	49.4	9.1	442	9	AA552253 nk06d09.s
33	49.4	9.1	463	9	AI926615 wk48e03.x
34	49.4	9.1	464	9	AA552098 nk05e01.s
35	49.4	9.1	492	9	AI802703 wf17d01.x
36	49.4	9.1	495	9	AI925615 wk34c12.x
37	49.4	9.1	523	9	AA573762 nk07c08.s
38	49.4	9.1	530	9	AA573823 nk08a08.s
39	49.4	9.1	535	9	AA573811 nk07n05.s
40	49.4	9.1	537	9	AA573949 nk09f07.s
41	49.4	9.1	540	9	AA573904 nk09p04.s
42	49.4	9.1	618	9	AA573910 nk09b11.s
43	49.4	9.0	118	9	AI919553 tp23a09.x
44	49.4	9.0	725	9	AI346914 qp59c05.x
45	47.8	8.8	178	14	BM768995 K-EST0052

ALIGNMENTS

RESULT 1
AI393251
LOCUS
DEFINITION
AI393251 478 bp mRNA linear EST 30-MAR-1999
t909b12.x1 NCI CGAP CELL Homo sapiens CDNA clone IMAGE:2108255.3
similar to SW:IECG_CROAT P21963 GALACTOSE-SPECIFIC LECTIN. ; mRNA
sequence.
ACCESSION
AI393251 GI:4222798
VERSION
AI393251.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alladeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 577 Std Error: 0.00

|||||
Db 8 ACACAAATGGTTATTAAAGAAATGTATGGCCCAATCATCAACCTGCAAGG--ATTCTACT 64
QY 61 GTTAAGCCTTCCTATGTGCCAAGAGAGAAACAGACATGAGCTTG 107
65 GGTAACCTTCCTATGTGCCCAAGAGAAACACACAGAGAGTTGACTG 111
RESULT 4
LOCUS A1470732 218 bp mRNA linear EST 13-APR-1999
DEFINITION t316f09.x1 NCI_CGAP_Gas4 Homo sapiens CDNA clone IMAGE:2141705 3',
ACCESSION A1470732
VERSION A1470732.1 GI:4332822
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 218)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR Gene Index
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrp/image/image.html
Insert length: 1005 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 170.
FEATURES
source
1..218
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2141705"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signal ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
BASE COUNT 62 a 32 c 54 g 70 t
ORIGIN
Query Match 9.1%; Score 49.4; DB 9; Length 218;
Best Local Similarity 72.9%; Pred. No. 0.00033;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
QY 1 ACACAAATGGTTATTAAAGAAATGTATGGCCCAATCAACCAAGAGATTCTACATG 60
|||||
Db 32 ACACAAATGGTTATTAAAGAAATGTATGGCCCAATCAACCTGCAAGG--ATTCTACT 88
QY 61 GTTAAGCCTTCCTATGTGCCAAGAGAGAAACAGACATGAGCTTG 107
65 GGTAACCTTCCTATGTGCCCAAGAGAAACACACAGAGAGTTGACTG 115
RESULT 5
LOCUS AA535703 250 bp mRNA linear EST 21-AUG-1997
DEFINITION n188c09.s1 NCI_CGAP_Co3 Homo sapiens CDNA clone IMAGE:926992 3',
ACCESSION AA535703
VERSION AA535703
KEYWORDS mRNA sequence.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 259)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR Gene Index
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

VERSION AA535703.1 GI:2279956
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 250)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR Gene Index
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrp/image/image.html
Seq primer: -40m13 fwd. RT from Amersham.
FEATURES
source
1..250
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:926992"
/clone_lib="NCI_CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/note="Vector: pT73d-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - Oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library went through one round of
normalization."
BASE COUNT 70 a 47 c 64 t
ORIGIN
Query Match 9.1%; Score 49.4; DB 9; Length 250;
Best Local Similarity 72.9%; Pred. No. 0.00036;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
QY 1 ACACAAATGGTTATTAAAGAAATGTATGGCCCAATCAACCAAGAGATTCTACATG 60
|||||
Db 5 ACACAAATGGTTATTAAAGAAATGTATGGCCCAATCAACCTGCAAGG--ATTCTACT 61
QY 61 GTTAAGCCTTCCTATGTGCCAAGAGAGAAACAGACATGAGCTTG 107
65 GGTAACCTTCCTATGTGCCCAAGAGAAACACACAGAGAGTTGACTG 108
RESULT 6
LOCUS AA582738 259 bp mRNA linear EST 25-SEP-1997
DEFINITION n39a03.s1 NCI_CGAP_GCS Homo sapiens CDNA clone IMAGE:1086220 3',
ACCESSION AA582738
VERSION AA582738
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 259)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR Gene Index
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert length: 1289 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 234.

FEATURES

source

1. 259

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1086220"

/clone_lib="NCI-CGAP_GCS"

/tissue_type="germ cell tumor"

/lab_host="SOLR (kanamycin resistant)"

/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"

: Cloned unidirectionally. Primer: Oligo dT. Mixed germ

cell tumors. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3'

adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average

Insert size: 0.7 kb."

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BASE COUNT

72 a 50 c 71 g 66 t

ORIGIN

1. 259

Query Match

9.1%; Score 49.4; DB 9; Length 259;

Best Local Similarity

72.9%; Pred. No. 0.00037;

Matches

78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

ACCESSION

AI282560

LOCUS

AI282560

DEFINITION

AI282560.1 GI:3920793

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE

1 (bases 1 to 280)

JOURNAL

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact:

Robert Strausberg, Ph.D.

Tissue Procurement:

Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation:

Life Technologies, Inc.

DNA Sequencing by:

Washington University Genome Sequencing Center

Clone distribution:

NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert length:

594 Std Error: 0.00

Seq primer:

-40UP from Gibco

High quality sequence stop:

268.

Location/Qualifiers

1. 280

FEATURES

source

1. 280

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1979740"

/clone_lib="NCI-CGAP_Gas4"

/tissue_type="poorly differentiated adenocarcinoma with

signet ring cell features"

/lab_host="DH10B"

/note="Organ: Stomach; Vector: PCMV-SPO86; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.69 kb. Life Technologies catalog #:

11549-011"

BASE COUNT

77 a 55 c 75 g 73 t

ORIGIN

1. 279

REFERENCE
1 (bases 1 to 293)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

BASE COUNT 92 a 59 c 93 g 76 t 1 others
ORIGIN

Query Match 9.1%; Score 49.4; DB 9; Length 321;
Best Local Similarity 72.9%; Pred. No. 0.00041;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

Db 1 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTTCTACATG 60
7 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGG---ATTCTACT 63

QY 61 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGTTG 107
64 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGTTG 110

RESULT 14
LOCUS AA612996 321 bp mRNA linear EST 03-OCT-1997
DEFINITION ng3b01.s1 NCI_CGAP_Col0 Homo sapiens cDNA clone IMAGE:1146217 3',
mRNA sequence.
ACCESSION AA612996
VERSION AA612996.1 GI:2464034
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 160.
Location/Qualifiers
1. 321
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1146217"
/clone_lib="NCI_CGAP_Col0"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldic (N-Soares4). "

BASE COUNT 93 a 58 c 96 g 74 t
ORIGIN

Query Match 9.1%; Score 49.4; DB 9; Length 321;
Best Local Similarity 72.9%; Pred. No. 0.00041;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

Db 1 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTTCTACATG 60
5 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGG---ATTCTACT 61

QY 61 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGTTG 107

Db 62 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGTTG 108

RESULT 15
LOCUS AA584947 345 bp mRNA linear EST 26-SEP-1997
DEFINITION aa1808.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086423 3',
mRNA sequence.
ACCESSION AA584947
VERSION AA584947.1 GI:2367727
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 345)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrp/image/image.html
Insert length: 910 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 283.
Location/Qualifiers
1. 345
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1086423"
/clone_lib="NCI_CGAP_GC5"
/tissue_type="germ cell tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site: 1: EcoRI; Site 2: XhoI
; Cloned unidirectionally. Primer: Oligo dT. Mixed germ
cell tumors. 5' adaptor sequence: 5' GAATTCGGCAGCAG 3' 3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' Average
insert size: 0.7 kb."

BASE COUNT 100 a 63 c 102 g 80 t
ORIGIN

Query Match 9.1%; Score 49.4; DB 9; Length 345;
Best Local Similarity 72.9%; Pred. No. 0.00043;
Matches 78; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

Db 1 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGAGGATTTCTACATG 60
8 ACACATGCTTTTAAAGATGTATGGCCCATCAACCAAGG---ATTCTACT 64

QY 61 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGTTG 107
65 GTAAGCCTTCTATGTGCCAAGAGAAACAGACATGAGTTG 111

Search completed: March 21, 2003, 19:11:43
Job time: 2625.1 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 11:56:08 ; Search time 2534.09 Seconds

(without alignments)
4490.451 Million cell updates/sec

Title: US-09-823-101-11

Perfect score: 391

Sequence: 1 actctcaatcaacaagacc.....taagagacgaagaaagcatgc 391

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	391	100.0	391	6	AX338098	AX338098 Sequence
2	145.4	37.2	165493	2	AC018876	AC018876 Homo sapi
3	145.4	37.2	166207	9	AC091135	AC091135 Homo sapi
4	87.8	22.5	7218	6	166494	166494 Sequence 14
5	71	18.2	148825	2	AC105566	AC105566 Rattus no
6	67.8	17.3	144050	2	AC027566	AC027566 Homo sapi
7	67.8	17.3	144569	9	AL139001	AL139001 Human DNA
8	67.2	17.2	170519	2	AC093390	AC093390 Rattus no
9	66.4	17.0	168710	9	AC096763	AC096763 Homo sapi
10	65.6	16.8	116530	2	AP001957	AP001957 Homo sapi
11	65.6	16.8	123044	9	AC107381	AC107381 Homo sapi
12	65.4	16.7	110000	2	AC096324_0	AC096324 Rattus no
13	65.4	16.7	131070	9	AL353744	AL353744 Human DNA
14	65.4	16.7	158869	2	AC095500	AC095500 Rattus no
15	64.4	16.5	269296	2	AC103331	AC103331 Rattus no
16	64.2	16.4	116530	2	AP001957	AP001957 Homo sapi
17	64.2	16.4	123044	9	AC107381	AC107381 Homo sapi
18	63.8	16.3	96201	9	AC079601	AC079601 Homo sapi
19	63.8	16.3	173394	9	AC025040	AC025040 Homo sapi
20	63.8	16.3	183204	2	AC018906	AC018906 Homo sapi
21	63.8	16.3	188314	9	AC009494	AC009494 Homo sapi
22	63.6	16.3	320781	2	AC110095	AC110095 Rattus no
23	63.2	16.2	76028	9	AL451129	AL451129 Human DNA
24	63.2	16.2	157068	9	AL591416	AL591416 Human DNA
25	63	16.1	151678	2	AC115452	AC115452 Rattus no
26	62.8	16.1	47972	9	AL391843	AL391843 Human DNA
27	62.8	16.1	165408	2	AC107532	AC107532 Rattus no
28	62.6	16.0	162393	2	AC111746	AC111746 Rattus no
29	62.6	16.0	175256	2	AC114249	AC114249 Rattus no
30	62.4	16.0	123007	2	AC094437	AC094437 Rattus no
31	62	15.9	36323	2	AC009190	AC009190 Homo sapi
32	62	15.9	230787	2	AC115478	AC115478 Rattus no
33	61.6	15.8	18807	9	AC073375	AC073375 Homo sapi
34	61.6	15.8	69917	9	AC107056	AC107056 Homo sapi
35	61.6	15.8	73078	2	AC122132	AC122132 Homo sapi
36	61.6	15.8	127565	2	AL161611	AL161611 Homo sapi
37	61.6	15.8	165404	2	AC084119	AC084119 Homo sapi
38	61.6	15.8	166151	9	AC068723	AC068723 Homo sapi
39	61.6	15.8	169418	2	AC026628	AC026628 Homo sapi
40	61.2	15.7	94829	9	AL357272	AL357272 Human DNA
41	61.2	15.7	156787	2	AC034141	AC034141 Homo sapi
42	61.2	15.7	182600	2	AC034126	AC034126 Homo sapi
43	60.8	15.5	62894	2	AC113467	AC113467 Mus muscu
44	60.8	15.5	92749	2	AC097398	AC097398 Rattus no
45	60.8	15.5	134449	2	AC069049	AC069049 Homo sapi

ALIGNMENTS

RESULT 1	AX338098	391 bp	DNA	linear	PAT 09-JAN-2002
LOCUS	AX338098				
DEFINITION	Sequence 11 from Patent WO0175169.				
ACCESSION	AX338098				
VERSION	AX338098.1	GI:18128729			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Pluta,J., Chen,S.Y., Hu,P., Recipon,H. and Macina,R.A.				
	Compositions and methods for diagnosing, monitoring, staging,				
	imaging and treating stomach cancer				

JOURNAL Patent: WO 0175169-A 11 11-OCT-2001;
Diadexus, Inc. (US)
FEATURES Location/Qualifiers
Source 1..391
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 151 a 81 c 112 g 47 t
ORIGIN

Query Match 100.0% Score 391; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 7.1e-86;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCTTCATCAACAAGACCTGATGCAAAAACAGAAAAGGGAGAGATGTGAGGATCAG 60
1 ACTCTTCATCAACAAGACCTGATGCAAAAACAGAAAAGGGAGAGATGTGAGGATCAG 60
DB 1
QY 61 TCAGAGTGTGGGCTTCACAGAGTGAGCTTAATGAGGCTCTCTCAAGTTCTGTAATAAT 120
61 TCAGAGTGTGGGCTTCACAGAGTGAGCTTAATGAGGCTCTCTCAAGTTCTGTAATAAT 120
DB 61
QY 121 AACACAGTAAGCAGTCACTAACAACAAAAAAGGGGTTGGGG 180
121 AACACAGTAAGCAGTCACTAACAACAAAAAAGGGGTTGGGG 180
DB 121 AACACAGTAAGCAGTCACTAACAACAAAAAAGGGGTTGGGG 180
QY 181 GCGGGGCCCCCTCCGCCATTCGCGGCGTGTGTCCCGTGAAAAAGGGCCCAAT 240
181 GCGGGGCCCCCTCCGCCATTCGCGGCGTGTGTCCCGTGAAAAAGGGCCCAAT 240
DB 181 GCGGGGCCCCCTCCGCCATTCGCGGCGTGTGTCCCGTGAAAAAGGGCCCAAT 240
QY 241 ATACACTACTTCCCGGGGGGAGAAAAACAAAAACAAAAACAAAAACGGGGGGG 300
241 ATACACTACTTCCCGGGGGGAGAAAAACAAAAACAAAAACAAAAACGGGGGGG 300
DB 241 ATACACTACTTCCCGGGGGGAGAAAAACAAAAACAAAAACAAAAACGGGGGGG 300
QY 301 GGGACCCCGGGGACCAACAGAGGAGCCGGGGGAGAAAGGGGACCCGGCCCAAAA 360
301 GGGACCCCGGGGACCAACAGAGGAGCCGGGGGAGAAAGGGGACCCGGCCCAAAA 360
DB 301 GGGACCCCGGGGACCAACAGAGGAGCCGGGGGAGAAAGGGGACCCGGCCCAAAA 360
QY 361 CCCCCCAAAATTAAGAGCAGAAAAAGCATGC 391
361 CCCCCCAAAATTAAGAGCAGAAAAAGCATGC 391
DB 361 CCCCCCAAAATTAAGAGCAGAAAAAGCATGC 391

RESULT 2
AC018876/c 165493 bp DNA linear HTG 07-JUL-2000
LOCUS AC018876
DEFINITION Homo sapiens chromosome 18 clone RP11-289E15, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
AC018876
AC018876.4 GI:7230959
VERSION AC018876.4 GI:7230959
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 165493)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 165493)
Waterston, R.H.
Direct Submission
Submitted (21-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:6850795.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0289E15
----- Summary Statistics -----

Sequencing vector: M13; 81%
Sequencing vector: plasmid; 19%
Chemistry: Dye-primer ET; 81% of reads
Chemistry: Dye-terminator Big Dye; 19% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 157046 bases at least Q40
Consensus quality: 160223 bases at least Q30
Consensus quality: 161942 bases at least Q20
Insert size: 174000; agarose-fp
Insert coverage: 164793; sum-of-ctigs
Quality coverage: 4.36 in Q20 bases; agarose-fp
Quality coverage: 4.61 in Q20 bases; sum-of-ctigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1322: contig of 1322 bp in length ;
* 1323 1422: gap of unknown length
* 1423 8681: contig of 7259 bp in length
* 8682 8781: gap of unknown length
* 8782 28642: contig of 19861 bp in length
* 28643 28742: gap of unknown length
* 28743 46484: contig of 17742 bp in length
* 46485 46584: gap of unknown length
* 46585 68690: contig of 22106 bp in length
* 68691 68790: gap of unknown length
* 68791 99194: contig of 30404 bp in length
* 99195 99294: gap of unknown length
* 99295 131431: contig of 32137 bp in length
* 131432 131531: gap of unknown length
* 131532 165493: contig of 33962 bp in length.

FEATURES
Source 1..165493
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
/clone="RP11-289E15"

BASE COUNT 52008 a 30658 c 30763 g 51358 t 706 others
ORIGIN

Query Match 37.2% Score 145.4; DB 2; Length 165493;
Best Local Similarity 99.3%; Pred. No. 3.7e-26;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACTCTTCATCAACAAGACCTGATGCAAAAACAGAAAAGGGAGAGATGTGAGGATCAG 60
1 ACTCTTCATCAACAAGACCTGATGCAAAAACAGAAAAGGGAGAGATGTGAGGATCAG 60
DB 13795 ACTCTTCATCAACAAGACCTGATGCAAAAACAGAAAAGGGAGAGATGTGAGGATCAG 13736
QY 61 TCAGAGTGTGGGCTTCACAGAGTGAGCTTAATGAGGCTCTCTCAAGTTCTGTAATAAT 120
61 TCAGAGTGTGGGCTTCACAGAGTGAGCTTAATGAGGCTCTCTCAAGTTCTGTAATAAT 120
DB 13735 TCAGAGTGTGGGCTTCACAGAGTGAGCTTAATGAGGCTCTCTCAAGTTCTGTAATAAT 13676
QY 121 AACACAGTAAGCAGTCACTAACAACAAA 147
121 AACACAGTAAGCAGTCACTAACAACAAA 147
DB 13675 AACACAGTAAGCAGTCACTAACAATA 13649

RESULT 3
AC091135/c 166207 bp DNA linear PRI 12-DEC-2001
LOCUS AC091135
DEFINITION Homo sapiens chromosome 18, clone RP11-289E15, complete sequence.
AC091135
AC091135.9 GI:17530760
VERSION AC091135.9 GI:17530760
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 166207)
Birren,B., Linton,L., Nusbaum,C. and Lande,E.
Homo sapiens chromosome 18, clone RP11-289E15
Unpublished
2 (bases 1 to 166207)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barra,N., Bastien,V., Boguslavsky,L., Boukhalter,B., Brown,A.,
Camarat,J., Campiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K.,
Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., Larocque,K.,
Lamczak,J., Lander,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Margulis,N., Mathews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPeeters,R., Meldrum,J., Menus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Sougnier,C., Spencer,B., Strange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 166207)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Anderson,S., Barra,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarat,J., Campiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,K.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,
Lamczak,R., Lander,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Margulis,N., Mathews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPeeters,R., Meldrum,J.,
Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Sougnier,C., Spencer,B., Strange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (15-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 166207)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Anderson,S., Barra,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarat,J., Campiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,K.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,
Lamczak,R., Lander,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Margulis,N., Mathews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPeeters,R., Meldrum,J.,
Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Sougnier,C., Spencer,B., Strange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (12-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 12, 2001 this sequence version replaced g1:16931000.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: 112072
Center clone name: 289_E.15

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
/map="18"
/clone="RP11-289E15"
/clone_lib="RP11 Human Male BAC"
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repeat_region
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repeat_region
1819..2206
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3823..4258
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4263..4641
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4643..6104
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6105..6462
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6467..7047
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7048..7415
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7419..7723
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7820..8849
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8850..11798
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11811..12051
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12052..12343
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repeat_region
12344..12474
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12513..12591
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12629..13164
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13168..13474
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13475..13618
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repeat_region 13916, .13961
repeat_region /rpt_family="AT_rich"
repeat_region 14423, .14536
repeat_region /rpt_family="L2"
repeat_region 14550, .14789
repeat_region /rpt_family="LIMC/D"
repeat_region complement(14841, .15139)
repeat_region /rpt_family="L2"
repeat_region complement(16721, .16816)
repeat_region /rpt_family="LIMB7"
repeat_region 16932, .16978
repeat_region /rpt_family="MIR"
repeat_region 17398, .17454
repeat_region /rpt_family="L3"
repeat_region complement(17455, .17942)
repeat_region /rpt_family="L1PA16"
repeat_region 17943, .18109
repeat_region /rpt_family="L3"
repeat_region 18222, .18478
repeat_region /rpt_family="AluJb"
repeat_region 18356, .18682
repeat_region /rpt_family="L2"
repeat_region 19440, .19473
repeat_region /rpt_family="(A)n"
repeat_region 20646, .20763
repeat_region /rpt_family="MIR3"
repeat_region 21500, .21678
repeat_region /rpt_family="(7A)n"
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repeat_region /rpt_family="LIMC5"
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repeat_region /rpt_family="AluX"
repeat_region complement(23783, .23914)
repeat_region /rpt_family="MIR3"
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repeat_region 26974, .27018

Query Match 37.2%; Score 145.4; DB 9; Length 166207;
Best Local Similarity 99.3%; Pred. No. 3.7e-26;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACTCTCATCAACAGACCTGATGCAAAAACAGAAAAGGGAAGATGTGAGGATCAG 60
DB 62964 ACTCTCATCAACAGACCTGATGCAAAAACAGAAAAGGGAAGATGTGAGGATCAG 62905
OY 61 TCAGAGTGGTGGCTTCAGAGTGGACTTAATAGAGGCTGCTCAAGTTCTGTAATAAT 120
DB 62904 TCAGAGTGGTGGCTTCAGAGTGGACTTAATAGAGGCTGCTCAAGTTCTGTAATAAT 62845
OY 121 AAACAGAGTAACAGTCACTAACAAA 147
DB 62844 AAACAGAGTAACAGTCACTAACAAA 62818

RESULT 4
166494/c 166494 7218 bp DNA linear PAT 28-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION 166494
VERSION 166494.1 GI:2724471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
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REFERENCE 1 (bases 1 to 7218)
AUTHORS Dorer, F., Scheiflinger, F. and Falkner, F. Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES
source 1, 7218
BASE COUNT 1944 a 1491 c 1486 g 1929 t 368 others
ORIGIN

Query Match 22.5%; Score 87.8; DB 6; Length 7218;
Best Local Similarity 2.1%; Pred. No. 1.1e-11;
Matches 8; Conservative 252; Mismatches 119; Indels 0; Gaps 0;

OY 13 ACAAGACCTGATGCCAAAACAAAAGGGAAGATGTGAGGATCAGTGTGTGG 72
DB 1436 ACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1377
OY 73 GCTCAAGAGTGCATTAATGAGGCTGCTCAAGTCTGTAATAATAACAGATAAG 132
DB 1376 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1317
OY 133 CAGTCACTAACAAAAAATAAAAAAATAAAAAAAGGTTGGGCGCGGCCCT 192
DB 1316 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1257
OY 193 CCCCCCATTCGGGCGTGTGTCGCCGTGAAGAGGCGCCCAATATACACTGTTC 252
DB 1256 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1197
OY 253 CCGGGGGAGAGAAAACAAAACAAAACAAAACAAAACGGGGGGGACCCCGGG 312
DB 1196 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1137
OY 313 GACCAACAGGAGAGCGGGGGGAGAGAGGAGGAGCCCGGCCAAAACCCCAAAAT 372
DB 1136 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1077
OY 373 AAGAGAGAAAACATGCG 391
DB 1076 RRRRRRRRRATCGCAAGC 1058

RESULT 5
AC105566 148825 bp DNA linear HTG 13-JUL-2002
DEFINITION Rattus norvegicus clone CH230-250A15, *** SEQUENCING IN PROGRESS
ACCESSION AC105566
VERSION AC105566.2 GI:21736435
KEYWORDS HTG; HTGS PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 148825)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbata, U., Benton, J., Blinze, K., Blumenthal, R., Bonini, D.,
Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinik, H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escoto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
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*	57540	57639:	gap of unknown length
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*	58883	58982:	gap of unknown length
*	58983	60134:	contig of 1151 bp in length
*	60134	60233:	gap of unknown length
*	60234	61848:	contig of 1615 bp in length
*	61849	61948:	gap of unknown length
*	61949	63109:	contig of 1161 bp in length
*	63110	63209:	gap of unknown length
*	63210	64484:	contig of 1275 bp in length
*	64485	64584:	gap of unknown length
*	64585	66224:	contig of 1640 bp in length
*	66325	66324:	gap of unknown length
*	66325	67566:	contig of 1242 bp in length
*	67567	67666:	gap of unknown length
*	67667	69473:	contig of 1807 bp in length
*	69474	69573:	gap of unknown length
*	69574	71821:	contig of 2248 bp in length
*	71822	71921:	gap of unknown length
*	71922	74292:	contig of 2371 bp in length
*	74293	74392:	gap of unknown length
*	74393	76633:	contig of 2241 bp in length
*	76634	76733:	gap of unknown length
*	76734	78409:	contig of 1676 bp in length
*	78410	78509:	gap of unknown length
*	78510	79683:	contig of 1174 bp in length

Query Match	Best Local Similarity	Matches	72: Conservative	0: Mismatches	7: Indels	0: Gaps	0: Indels
Y 69	GTGGGCTCAAGAGTGGATTTATGAGGGCTGCTCAAGGTTCTCTAATATAATTAACAGAG	128	17.3%	Score 67.8; DB 2; Length 144070;			
Db 96064	GTGTGATCGAAGAGTGAGCTTATGGAACGTCTCAAGGTTCTGCAATTAATTAACAGAG	96005	91.1%	Pred. No. 1.2e-06;			
Y 129	TAAAGCAGTCTACTTAACAAA	147					
Db 96004	TAAAGCAGTCTACTTAACAAA	95986					
RESULT 7							
LOCUS	AL139001						
DEFINITION	Human DNA sequence from clone RP11-1G3 on chromosome 13q21.31-22.2.						
ACCESSION	AL139001						
VERSION	AL139001.14						
KEYWORDS	HTG.						
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
TITLE	1 (bases 1 to 144569)						
JOURNAL	Blakey, S.						
COMMENT	Submitted (16-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk						
	On Jul 14, 2000 this sequence version replaced gi:8977625.						
	During sequence assembly data is compared from overlapping clones.						
	Where differences are found these are annotated as variations						
	together with a note of the overlapping clone name. Note that the						
	validation annotation may not be found in the sequence submission						

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone comp15 of human chromosome 13, constructed by the Sanger Centre chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/MGP/Chr13>

Rp11-1G3 is from the library RPc1-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:PBACE3.6>

This sequence is the entire insert of clone Rp11-1G3 The true left end of clone Rp11-77P3 is at 95860 in this sequence.

Location/Qualifiers

URS	Location/Qualifiers
source	1..144569 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="13" /map="q21..31-22..2" /clone="Rp11-1G3" /clone_11b="RPC1-11.1" 1..575
misc_feature	/note="match: GSS: Em:AQ351418" 26..359
misc_feature	/note="match: GSS: Em:B48369" 974..1050
repeat_region	/note="T1Pv2 repeat: matches 6068..6144 of consensus" 1408..1532
repeat_region	/note="FLM_A repeat: matches 1..127 of consensus" 1604..1891
misc_feature	/note="AluX repeat: matches 1..293 of consensus" complement(2188..2914)
misc_feature	/note="match: GSS: Em:AQ374372" 2936..3614
misc_feature	/note="match: GSS: Em:AQ630026" 2938..3252
misc_feature	/note="match: GSS: Em:AQ546196" complement(3798..4375)
repeat_region	/note="match: GSS: Em:AQ321738 match: STRS: Em:G56702" 4503..5655
repeat_region	/note="Finger3b repeat: matches 2..1231 of consensus" 6474..6603
repeat_region	/note="66 copies 2 mer tt 59% conserved" 6567..6641
repeat_region	/note="3 copies 25 mer 80% conserved" 7446..7757
repeat_region	/note="AluX repeat: matches 1..312 of consensus" 8327..8620
misc_feature	/note="AluY repeat: matches 1..294 of consensus" 10318..10789
repeat_region	/note="match: GSS: Em:AQ772324" 10471..10520
misc_feature	/note="2 copies 25 mer 98% conserved" 11384..11823
repeat_region	/note="match: GSS: Em:AQ580756" 11397..11677
repeat_region	/note="AluX repeat: matches 3..284 of consensus" 12460..12548
repeat_region	/note="MIR1 repeat: matches 103..200 of consensus" 13022..13097
repeat_region	/note="19 copies 4 mer at 80% conserved" 13043..13096

repeat_region /note="9 copies 6 mer tatata 90% conserved"
13096..13135
repeat_region /note="20 copies 2 mer ag 85% conserved"
16504..16531
repeat_region /note="14 copies 2 mer ac 96% conserved"
16565..16600
repeat_region /note="18 copies 2 mer at 80% conserved"
18654..18767
repeat_region /note="MER91C repeat: matches 12..130 of consensus"
18773..18946
repeat_region /note="L2 repeat: matches 2027..2231 of consensus"
19011..19173
repeat_region /note="L2 repeat: matches 2457..2609 of consensus"
19818..19898
repeat_region /note="MIR repeat: matches 73..154 of consensus"
20754..20845
repeat_region /note="MER45C repeat: matches 1..91 of consensus"
20870..21150
repeat_region /note="AluSp repeat: matches 4..285 of consensus"
21177..21484
repeat_region /note="AluSq repeat: matches 2..308 of consensus"
21509..21739
repeat_region /note="MER45B repeat: matches 105..327 of consensus"
21853..22555
repeat_region /note="MER45C repeat: matches 183..903 of consensus"
22619..22705
repeat_region /note="MIR repeat: matches 75..164 of consensus"
22830..22921
repeat_region /note="46 copies 2 mer ta 62% conserved"
22967..23000
repeat_region /note="17 copies 2 mer ac 97% conserved"
22969..23000
repeat_region /note="8 copies 4 mer acac 100% conserved"
24902..25090
repeat_region /note="MIR repeat: matches 18..211 of consensus"
28576..28714
repeat_region /note="WSTC repeat: matches 259..393 of consensus"
28723..28858
repeat_region /note="L1ME repeat: matches 2132..2271 of consensus"
29020..29069
repeat_region /note="L1R40A repeat: matches 459..509 of consensus"
29799..30071
repeat_region /note="MULTI repeat: matches 1..267 of consensus"
30803..31026
repeat_region /note="MER33 repeat: matches 57..302 of consensus"
31379..31487
repeat_region /note="L2 repeat: matches 2633..2750 of consensus"
32235..32688
misc_feature /note="match: GSS: Em:A0892477"
35573..35698
repeat_region /note="FRAM repeat: matches -5..120 of consensus"
35700..35973
misc_feature /note="Tandem repeat. Contains forced join. Assembly is confirmed by restriction digest."
35735..35909
repeat_region /note="7 copies 25 mer 74% conserved"
35751..35914
repeat_region /note="41 copies 4 mer ttct 73% conserved"
35752..35915
repeat_region /note="82 copies 2 mer tt 71% conserved"
35918..36016
repeat_region /note="FLAM_C repeat: matches 6..110 of consensus"
36506..36933
repeat_region /note="MULTI repeat: matches 65..474 of consensus"
37087..37387
repeat_region /note="AluSc repeat: matches 1..295 of consensus"
37485..37730
repeat_region /note="MULTI repeat: matches 24..270 of consensus"
38868..39224
repeat_region /note="THE1B repeat: matches 1..364 of consensus"
39225..40781
repeat_region /note="THE1B-INTERNAL repeat: matches 11..1580 of consensus"

repeat_region 40786..41150
/note="THE1B repeat: matches 1..364 of consensus"
repeat_region 41193..41261
/note="L1R28 repeat: matches 1..70 of consensus"
repeat_region 41263..41517
/note="L1R27 repeat: matches 201..576 of consensus"
repeat_region 41607..41752
/note="L1R27 repeat: matches 494..636 of consensus"
misc_feature /note="L1R27 repeat: matches 494..636 of consensus"
/note="match: GSS: Em:A0510993"
42771..43092
misc_feature /note="match: GSS: Em:B52827"
42776..43489
misc_feature /note="match: GSS: Em:AQ269328"
42809..43196
misc_feature /note="match: GSS: Em:AQ016365"
43167..43582
misc_feature /note="match: GSS: Em:AQ408187"
43167..43567
misc_feature /note="match: GSS: Em:AQ408146"
43176..43876
misc_feature /note="match: GSS: Em:AQ394839"
43857..43925
repeat_region /note="L1P48 repeat: matches 6091..6159 of consensus"
44302..44547
misc_feature /note="match: GSS: Em:AQ580520"
/note="match: GSS: Complement(49385..49684)
49481..49582
misc_feature /note="match: GSS: Em:AQ776034"
/note="AluSp/q repeat: matches 169..294 of consensus"
49701..50279
misc_feature /note="match: GSS: Em:A0608129"
49963..50269
repeat_region

Query Match 17.3% Score 67.8; DB 9; Length 144569;
Best Local Similarity 91.1%; Pred. No. 1.2e-06;
Matches 72; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 69 GTGGCTCAAGAGTGCATTAATGAGGCTGTCATCAAGCTTCGTATATAATAACACAG 128
Db 82724 GTGTGATCGAGAGTGCATTAATGAGAGCTTCGTCAATATAATAACACAG 82783

QY 129 TAAGCAGTCACTAACAAA 147
Db 82784 TAAGCAGTCACTAACATA 82802

RESULT 8
AC095390
LOCUS

AC095390 170519 bp DNA linear HTG 10-JUL-2002
Rattus norvegicus clone CH230-7C24, *** SEQUENCING IN PROGRESS ***
DEFINITION
70 unordered pieces.

ACCESSION
AC095390
VERSION
AC095390.3 GI:21716824
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 170519)
AUTHORS

Muzny,D.M., Adams,C., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarta,J., Benton,J., Blimie,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Bunay,C., Burch,P., Burkett,C., Buttrill,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Devilla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinu,H.H.,
Douthwaite,K.J., Drepper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Kervah,J., Kovar,C., Kravovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lorzdo,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,A., Nguyen,N., Moser,M., Neal,D., Newton,J., Newton,S., Ogut,M., Okunou,G., Nguyen,N., Nickerson,E., Nwokenkwu,S., Ogui,M., Okunou,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabot,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleczyk,R., Wocden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 170519)
Worley,K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 170519)
Worley,K.C.

Direct Submission
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 9, 2002 this sequence version replaced gi:17941844.

----- Genome Center -----
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: GCAY
Center clone name: CH230-7624
----- Summary Statistics -----
Sequencing vector: Plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127166 bases at least Q40
Consensus quality: 133375 bases at least Q30
Consensus quality: 138883 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length -----
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1055: contig of 1055 bp in length
* 1056 1155: gap of unknown length
* 1156 2308: contig of 1153 bp in length
* 2309 2408: gap of unknown length

2409 3466: contig of 1058 bp in length
* 3467 3566: gap of unknown length
* 3567 4871: contig of 1305 bp in length
* 4872 4971: gap of unknown length
* 4972 6028: contig of 1057 bp in length
* 6029 6129 7145: gap of unknown length
* 7146 7245: gap of unknown length
* 7246 8326: contig of 1081 bp in length
* 8327 8427 9473: gap of unknown length
* 8427 9473: contig of 1047 bp in length
* 9474 9573: gap of unknown length
* 9574 10639: contig of 1066 bp in length
* 10640 10739: gap of unknown length
* 10740 12038: contig of 1299 bp in length
* 12039 12138: gap of unknown length
* 12139 13485: contig of 1347 bp in length
* 13486 13585: gap of unknown length
* 13586 14858: contig of 1273 bp in length
* 14859 14958: gap of unknown length
* 14959 15981: contig of 1023 bp in length
* 15982 16081: gap of unknown length
* 16082 17443: contig of 1362 bp in length
* 17443 17543: gap of unknown length
* 17544 19746: contig of 2203 bp in length
* 19747 19846: gap of unknown length
* 19847 21076: contig of 1230 bp in length
* 21077 21176: gap of unknown length
* 21177 22433: contig of 1257 bp in length
* 22434 22533: gap of unknown length
* 22534 24170: contig of 1637 bp in length
* 24171 24270: gap of unknown length
* 24271 25626: contig of 1356 bp in length
* 25627 25726: gap of unknown length
* 25727 26795: contig of 1949 bp in length
* 26796 27775: gap of unknown length
* 27776 29132: contig of 1357 bp in length
* 29133 29232: gap of unknown length
* 29233 30445: contig of 1213 bp in length
* 30446 30545: gap of unknown length
* 30546 31715: contig of 1170 bp in length
* 31716 31815: gap of unknown length
* 31816 33291: contig of 1476 bp in length
* 33292 33391: gap of unknown length
* 33392 34552: contig of 1161 bp in length
* 34553 34652: gap of unknown length
* 34653 35762: contig of 1110 bp in length
* 35763 35862: gap of unknown length
* 35863 37152: contig of 1290 bp in length
* 37153 37252: gap of unknown length
* 37253 38449: contig of 1197 bp in length
* 38450 38549: gap of unknown length
* 38550 40042: contig of 1493 bp in length
* 40043 40142: gap of unknown length
* 40143 41190: contig of 1048 bp in length
* 41191 41290: gap of unknown length
* 41291 43534: contig of 2244 bp in length
* 43535 43634: gap of unknown length
* 43635 45519: contig of 1885 bp in length
* 45520 45619: gap of unknown length
* 45620 47291: contig of 1672 bp in length
* 47292 47391: gap of unknown length
* 47392 48691: contig of 1300 bp in length
* 48692 48791: gap of unknown length
* 48792 49802: contig of 1011 bp in length
* 49803 49902: gap of unknown length
* 49903 51992: contig of 2090 bp in length
* 51993 52092: gap of unknown length
* 52093 53647: contig of 1555 bp in length
* 53648 53747: gap of unknown length
* 53748 55085: contig of 1338 bp in length
* 55086 55185: gap of unknown length
* 55186 57533: contig of 2348 bp in length

COMMENT

REFERENCE
AUTHORS
TITLE
JOURNAL

```

* 57534 57633: gap of unknown length
* 57634 59083: contig of 1450 bp in length
* 59084 59183: gap of unknown length
* 59184 60810: contig of 1627 bp in length
* 60811 60911: gap of unknown length
* 60911 62159: contig of 1248 bp in length
* 62159 62259: gap of unknown length
* 62259 63966: contig of 1708 bp in length
* 63967 64067: gap of unknown length
* 64067 66129: contig of 2063 bp in length
* 66130 66230: gap of unknown length
* 66230 67945: contig of 1716 bp in length
* 67946 68046: gap of unknown length
* 68046 69815: contig of 1770 bp in length
* 69816 72258: contig of 2343 bp in length
* 72259 72359: gap of unknown length
* 72359 74521: contig of 2162 bp in length
* 74521 74621: gap of unknown length
* 74621 77335: contig of 2714 bp in length
* 77335 77434: gap of unknown length
* 77435 80466: contig of 3032 bp in length
* 80467 80567: gap of unknown length
* 80567 83709: contig of 3142 bp in length
* 83709 83808: gap of unknown length
* 83809 86115: contig of 2307 bp in length
* 86116 86216: gap of unknown length
* 86216 88293: contig of 2078 bp in length
* 88294 88393: gap of unknown length
* 88394 90604: contig of 2211 bp in length

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Query Match 17.2% Score 67.2; DB 2; Length 170519;
 Best Local Similarity 50.9%; Pred. No. 1.6e-06;
 Matches 114; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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OY 143 CAAAAAAAAAAAAAAAAAAGGTTGGGGGCGGCCCTCCCTCCCTCCCAT 202
    |||||||
DB 4217 CAAAAAAAAAAAAAAAAAAGGGGTGGGGGGGGGGGGGGGGGGGGGGGG 4276
    |||||||
OY 203 TCCGGGCGTGTGTCCCGCTGAAAAAGGGGCCCAATATACATGTTCCCGGGGGA 262
    |||||||
DB 4277 CCCCCAATTTTTTTTTNNNNNNNNNNNNCCCGCCCCCCCCCCCCCCCCCGC 4336
    |||||||
OY 263 GAAAAACAAAAAACAAAAAACCGGGGGGGGACCCCGGGGACCAACAGG 322
    |||||||
DB 4337 CCGGCNNAAAAAAGAAAAAACCCACACCCNNNNNGGGCCCCGGGAGAGGGGGG 4396
    |||||||
OY 323 GGAGCGGGGGGGAAGAGCGGCCCGCGCCAAACCCCGC 366
    |||||||
DB 4397 GGGGGGGGGGGGGGGGGGGGGGGGCGGNNNNNNNNNNCC 4440
    |||||||

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RESULT 9
 AC096763
 LOCUS AC096763 168710 bp DNA linear PRI 01-MAR-2002
 DEFINITION Homo sapiens BAC clone RP11-625A6 from 4, complete sequence.
 ACCESSION AC096763 AC025523
 VERSION AC096763.2 GI:18042483
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 168710)
 AUTHORS Sulston J.E. and Waterston R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 9847074
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 168710)
 AUTHORS Swearingen S. and Cotton M.
 TITLE The sequence of Homo sapiens BAC clone RP11-625A6
 JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 168710)
 AUTHORS Waterston R.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 168710)
 AUTHORS Waterston R.H.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 168710)
 AUTHORS Waterston R.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jan 3, 2002 this sequence version replaced gi:15741642.
 COMMENT

 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@wustl.wustl.edu

 Center project name: H_NH0625A06
 Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping Information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
 VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the right is AC015631. Actual start of this clone is at base position 1 of RP11-625A6.

The sequence of AC025523 has been incorporated into AC096763.

FEATURES
 source
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 /db_xref="taxon:9606"
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                    16733..17098
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                    19542..19564
repeat_region      /rpt_family="(CAG)n"
                    19909..19923
repeat_region      /rpt_family="MER2_type"
                    25582..26031
repeat_region      /rpt_family="ERV_K"
                    26037..26266
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repeat_region      /rpt_family="MER2_type"
                    26824..26866
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Best Local Similarity 98.5%; Pred. No. 2.6e-06;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      68 GGTGGGCTCAAGAGTGACTTAATGAGGGGCTGCTCAAGGTTCTGTAATTAATTAACAGA 127
        |||
Db      22817 GGTGGGCTCAAGAGTGACTTAATGAGGGGCTGCTCAAGGTTCTGTAATTAATTAACAGA 22876

QY      128 GTAAGCAG 135
        |||
Db      22877 GTAAGCAG 22884

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RESULT 10
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LOCUS
DEFINITION      Homo sapiens chromosome 4 clone 237569 map 4q22-q24, *** SEQUENCING
IN PROGRESS ***, 5 unordered pieces.
ACCESSION      AP001957
VERSION        AP001957.1 GI:7678847
KEYWORDS
SOURCE        HTG: HTGS-PHASE1.
ORGANISM      Homo sapiens
               Homo sapiens DNA, clone:237569.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 116530)
AUTHORS      Tsai,S.F.
TITLE        Direct Submision
JOURNAL      Submitted (28-APR-2000) Shih-Peng Tsai, National Yang-Ming
               University, Institute of Genetics, 155 Li-Rong St. Section 2,
               Peitou, Taipei, Taiwan 11221, Republic of China
               (E-mail: ympeisa@ym.edu.tw, URL: http://genome.ym.edu.tw/,
               Tel:886-2-28267043, Fax:886-2-28264930)
COMMENT      Gaps between the contigs are represented as 100 N.
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 5 contigs. The true order of the pieces
               * is not known and their order in this sequence record is

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* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 5872: contig of 5872 bp in length
 * 5873 5972: gap of 100 bp
 * 5973 18176: contig of 12204 bp in length
 * 18177 18276: gap of 100 bp
 * 18277 28627: contig of 10351 bp in length
 * 28628 28727: gap of 100 bp
 * 28728 42761: contig of 14034 bp in length
 * 42762 42861: gap of 100 bp
 * 42862 116530: contig of 73669 bp in length.
 * Location/Qualifiers
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 /db_xref="taxon:9606"
 /map="4q22-q24"
 /clone="2375G9"

BASE COUNT 38696 a 21933 c 21727 g 33774 t 400 others

ORIGIN

Query Match 16.8%; Score 65.6; DB 2; Length 116530;
 Best Local Similarity 76.9%; Pred. No. 4.2e-06;
 Matches 80; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 68 GGTGGGCTCAAGAGTGCTTAATGAGGCTGCTCAAGTCTGTAATTAATTAACAGA 127
 Db 89779 GGTGGGCTCAAGAGTGCTTAATGAGGCTGCTCAAGTCTGTAATTAATTAACAGA 89720

QY 128 GTAAGCAGTCACTACCAAAAAAAAAAAAAAAAAAAG 171
 Db 89719 GTAAGCAGTCACTACCAATATGTGATGAGCTGAATGGAAG 89676

RESULT 11
 AC107381/C 123044 bp DNA linear PRI 21-FEB-2002
 LOCUS Homo sapiens BAC clone RP11-41F9 from 4, complete sequence.
 AC107381
 AC107381.2 GI:18464259
 HTG.
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 123044)
 Sulston, J.E. and Waterston, R.
 Toward a complete human genome sequence
 Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074

REFERENCE
 AUTHORS 2 (bases 1 to 123044)
 TITLE Shah, N., Hakenson, W. and Boyer, E.
 JOURNAL The sequence of Homo sapiens BAC clone RP11-41F9
 UNPUBLISHED (2001)
 REFERENCE 3 (bases 1 to 123044)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108 USA
 4 (bases 1 to 123044)
 Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (01-FEB-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE 5 (bases 1 to 123044)
 AUTHORS Waterston, R.
 TITLE Direct Submission

JOURNAL Submitted (21-FEB-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Feb 1, 2002 this sequence version replaced gi:18250108.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0041F09

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D.
 McPherson, Department of Genetics, Washington University, St. Louis
 MO. For additional information about the map position of this
 sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RP11-11 human BAC library was made from the blood of one male
 donor, as described by Osogawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
 Tateo, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
 approach for construction of bacterial artificial chromosome
 libraries. Genomics 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
 and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is AP001820. Actual end of this
 clone is at base position 123044 of RP11-41F9.

Sequence derived from one plasmid subclone, base position 22028 to
 22036.

FEATURES
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repeat_region	17572. .17945	/rpt_family="(CAAAA)n"
repeat_region	17946. .19553	/rpt_family="MaLR"
repeat_region	19358. .19897	/rpt_family="MaLR"
repeat_region	21467. .21538	/rpt_family="MaLR"
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repeat_region	22015. .22034	/rpt_family="S(CAA)n"
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repeat_region	22882. .22982	/rpt_family="L1"
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misc_feature	23986. .24151	/note="match to EST BG204777 (NID:g13726464) "
misc_feature	23987. .24151	/note="match to EST AA809486 (NID:g2878892) ob85c11.si"
misc_feature	23987. .24151	/note="match to EST BF931516 (NID:g12348840) "
misc_feature	23992. .24151	/note="match to EST BG189108 (NID:g13710795) "
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repeat_region	32031. .32135	/rpt_family="MIR"
repeat_region	32231. .33061	/rpt_family="L1"
repeat_region	37519. .37558	/rpt_family="(CA)n"
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REFERENCE	AUTHORS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	LOCUS	DEFINITION	HTG	DATE	STATUS	
1	(bases 1 to 385671)	AC096324	4	GI:21723482	HTGS_PHAISE1.	NC_009632.4	1	100000	100000	100000	100000	
2	Murphy, D.M., Adams, C., Alibrooks, S.L., Amaral, J., Barch, J., Boyle, S., Brive, M., Brown, E., Brown, M., Bryan, N.P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Day-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dim, H.H., Douthett, K.K., Drape, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escoto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabri, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J., Harris, K., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hughes, M., Hollway, C., Hollins, B., Homsl, J., Howard, S., Huber, J., Hulik, S., Hume, J., Jackson, L.E.,	AC096324_0	AC096324_1	AC096324_2	AC096324_3	AC096324	140 unorderd pieces.	AC096324	AC096324.4	GI:21723482	HTGS_PHAISE1.	NC_009632.4
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13	NC_009632.4	1	100000	100000	100000	100000	100000	100000	100000	100000	100000	
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17	NC_009632.4	1	100000	100000	100000	100000	100000	100000	100000	100000	100000	
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22	NC_009632.4	1	100000	100000	100000	100000	100000	100000	100000	100000	100000	
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Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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 Rivers,M., Rojas,A., RojudoKan,I., Rolfe,M., Ruiz,S., Saverly,G.,
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 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
 Welstock,G. and Gibbs,R.

 Direct Submission
 Unpublished
 2 (bases 1 to 385671)
 Worley,K.C.

 Direct Submission
 Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 385671)
 Worley,K.C.

 Direct Submission
 Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 10, 2002 this sequence version replaced gi:17944023.

 Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc.helpebcm.tmc.edu

 Project Information
 Center project name: GEXV
 Center clone name: CH230-72D6

 Summary Statistics
 Sequencing vector: Plasmid:
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap: version 0.990329
 Consensus quality: 220322 bases at least Q40
 Consensus quality: 223244 bases at least Q30
 Consensus quality: 225362 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 140 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
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 * 1110 1209: gap of unknown length
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 * 3422 3521: gap of unknown length
 * 3522 4585: contig of 1064 bp in length
 * 4586 4685: gap of unknown length
 * 4686 5866: contig of 1181 bp in length
 * 5867 5966: gap of unknown length
 *
 * 5967 7186: contig of 1220 bp in length
 * 7187 7286: gap of unknown length
 * 7287 8318: contig of 1032 bp in length
 * 8319 8418: gap of unknown length
 * 8419 9793: contig of 1375 bp in length
 * 9794 9893: gap of unknown length
 * 9894 10924: contig of 1031 bp in length
 * 10925 11024: gap of unknown length
 * 11026 12197: contig of 1173 bp in length
 * 12198 12298: gap of unknown length
 * 12299 13709: contig of 1412 bp in length
 * 13710 13809: gap of unknown length
 * 13810 14929: contig of 1120 bp in length
 * 14930 15029: gap of unknown length
 * 15030 16125: contig of 1096 bp in length
 * 16126 16225: gap of unknown length
 * 16226 17261: contig of 1036 bp in length
 * 17262 17361: gap of unknown length
 * 17362 18578: contig of 1217 bp in length
 * 18579 18678: gap of unknown length
 * 18679 19961: contig of 1283 bp in length
 * 19962 20061: gap of unknown length
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 * 21266 22417: contig of 1152 bp in length
 * 22418 22517: gap of unknown length
 * 22519 23664: contig of 1147 bp in length
 * 23665 23765: gap of unknown length
 * 23766 25137: contig of 1373 bp in length
 * 25138 25237: gap of unknown length
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 * 26353 27491: contig of 1139 bp in length
 * 27492 27591: gap of unknown length
 * 27592 28662: contig of 1071 bp in length
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 * 31811 31910: gap of unknown length
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 * 33118 33217: gap of unknown length
 * 33219 34597: contig of 1380 bp in length
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 * 34698 36026: contig of 1329 bp in length
 * 36027 36126: gap of unknown length
 * 36127 37156: contig of 1030 bp in length
 * 37157 37256: gap of unknown length
 * 37257 38344: contig of 1088 bp in length
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 * 48888 50246: contig of 1359 bp in length
 * 50247 50346: gap of unknown length
 * 50347 51386: contig of 1040 bp in length
 * 51387 51486: gap of unknown length
 * 51487 52504: contig of 1018 bp in length
 * 52505 52604: gap of unknown length
 * 52605 53870: contig of 1266 bp in length

repeat_region 14253. 14553
/note="AluIo repeat: matches 1. .299 of consensus"
repeat_region 14554. 14924
/note="L1MB1 repeat: matches 5753. .6140 of consensus"
repeat_region 15198. 15508
/note="AluIb repeat: matches 3. .309 of consensus"
repeat_region 15514. 15828
/note="AluIo repeat: matches 1. .312 of consensus"
repeat_region 16201. 16234
/note="17 copies 2 mer ga 97% conserved"
repeat_region 16470. 16592
/note="MIR repeat: matches 105. .234 of consensus"
repeat_region 18005. 18112
/note="L2 repeat: matches 2591. .2710 of consensus"
repeat_region 18395. 18472
/note="L2 repeat: matches 2208. .2290 of consensus"
repeat_region 18479. 18783
/note="MER1B repeat: matches 31. .337 of consensus"
repeat_region 18832. 19390
/note="L2 repeat: matches 1490. .2090 of consensus"
repeat_region 20113. 20154
/note="21 copies 2 mer tt 90% conserved"
repeat_region 20736. 20904
/note="MSTB repeat: matches 1. .158 of consensus"
repeat_region 21025. 21471
/note="MER3 repeat: matches 1. .448 of consensus"
repeat_region 23402. 23740
/note="L1PA13 repeat: matches 5822. .6155 of consensus"
repeat_region 24264. 24289
/note="13 copies 2 mer gt 92% conserved"
repeat_region 24489. 24934
/note="MER31B repeat: matches 3. .539 of consensus"
repeat_region 24935. 24956
/note="11 copies 2 mer tt 100% conserved"
repeat_region 25833. 25958
/note="MIR repeat: matches 81. .220 of consensus"
repeat_region 26176. 26374
/note="AluIb repeat: matches 85. .220 of consensus"
repeat_region 26681. 32690
/note="L1PA5 repeat: matches 3. .6143 of consensus"
repeat_region 33417. 33512
/note="FLAM-A repeat: matches 3. .101 of consensus"
repeat_region 35300. 35609
/note="AluSg repeat: matches 1. .304 of consensus"
repeat_region 35613. 35957
/note="L1MA2 repeat: matches 5932. .6308 of consensus"
repeat_region 35971. 41466
/note="L1PA10 repeat: matches 924. .6159 of consensus"
repeat_region 41467. 42297
/note="LTR1 repeat: matches 1. .785 of consensus"
repeat_region 42298. 43197
/note="L1PA10 repeat: matches 20. .924 of consensus"
repeat_region 43198. 43837
/note="L1MA3 repeat: matches 5314. .5552 of consensus"
repeat_region 44383. 44552
/note="FRAM repeat: matches -6. .164 of consensus"
repeat_region 44921. 45108
/note="L2 repeat: matches 1683. .1883 of consensus"
repeat_region 45621. 45857
/note="L2 repeat: matches 2157. .2397 of consensus"
repeat_region 46044. 46284
/note="L1MA7 repeat: matches 5318. .5557 of consensus"
repeat_region 46288. 46407
/note="LTR1 repeat: matches 667. .783 of consensus"
repeat_region 46464. 46793
/note="LTR1 repeat: matches 324. .660 of consensus"
repeat_region 46579. 46836
/note="LTR28 repeat: matches 350. .603 of consensus"
repeat_region 47105. 47742
/note="L1MA7 repeat: matches 5572. .6278 of consensus"
repeat_region 48685. 48782
/note="MIR repeat: matches 48. .146 of consensus"
repeat_region 49246. 49441

repeat_region /note="L1PA2 repeat: matches 5549. .6144 of consensus"
repeat_region 49600. 49908
/note="L1ME3A repeat: matches 5526. .5855 of consensus"
repeat_region 50299. 50641
/note="L1MA5 repeat: matches 732. .1100 of consensus"
repeat_region 50642. 50934
/note="AluIb repeat: matches 1. .293 of consensus"
repeat_region 50935. 51088
/note="L1MA5 repeat: matches 1100. .1252 of consensus"
repeat_region 51171. 51845
/note="L1MA5 repeat: matches 1356. .2016 of consensus"
repeat_region 51846. 51986
/note="L1PA14 repeat: matches 6009. .6149 of consensus"
repeat_region 51987. 56148
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repeat_region 57190. 57661
/note="HAI1 repeat: matches 1178. .1666 of consensus"
repeat_region 57789. 58196
/note="L1 repeat: matches 4816. .5233 of consensus"
repeat_region 58332. 58443
/note="L2 repeat: matches 2588. .2705 of consensus"
repeat_region 59062. 59561
/note="L1 repeat: matches 4369. .4824 of consensus"
repeat_region 59873. 60755
/note="L1 repeat: matches 3427. .4369 of consensus"
repeat_region 60756. 61035
/note="AluIv repeat: matches 3. .284 of consensus"
repeat_region 61036. 61698
/note="L1 repeat: matches 2783. .3427 of consensus"
repeat_region 61703. 62228
/note="L1M4 repeat: matches 4333. .4846 of consensus"
repeat_region 62341. 62457
/note="L1MA8 repeat: matches 6150. .6270 of consensus"
repeat_region 62650. 62700

Query Match 16.7%; Score 65.4; DB 9; Length 131070;
Best Local Similarity 73.0%; Pred. No. 4.7e-06;
Matches 84; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 68 GCGGGCTCAAGAGGACTTAATGAGCGGCTGTCACAGCTTCTGTAATTAACGA 127
Db 119967 GGGGGCTCAAGAGGACTTAATGAGCGGCTGTCACAGCTTCTGTAATTAATGGA 120026
Qy 128 GTAAGCAGTCACTAACAAAAAAGAGGTTGGCGGC 182
Db 120027 GTAAGCAGTCACTAACAAAAAAGAGGTTGGCGGC 120081

RESULT 14
AC095500 158869 bp DNA linear HTG 10-JUL-2002
LOCUS Rattus norvegicus clone CH230-7P12, *** SEQUENCING IN PROGRESS ***
DEFINITION 71 unordered pieces.
ACCESSION AC095500.3 GI:21716936
VERSION AC095500.3
KEYWORDS HTG; HTGS; PHASEL.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 158869)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbacia,J., Benton,J., Blinze,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathore,S.R., David,R., Davila,M.L., Davis,C., Day-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dim,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Correll,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lien,C., Liu,J., Liu,W., Loulseged,H., Lozodo,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., Mcleod,M.P., Meador,M., Mei,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,M., Moser,M., Neal,D., Newton,J., Newton,S., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonigbo,G., Otagunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,L., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleczky,R., Woden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

Unpublished
2 (bases 1 to 158869)
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 158869)
Worley K.C.
Direct Submission
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 9, 2002 this sequence version replaced gi:11942007.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCMD
Center clone name: CH230-7P12
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 88636 bases at least Q40
Consensus quality: 95512 bases at least Q30
Consensus quality: 100849 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see <http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft.data.html>).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 71 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1494: contig of 1494 bp in length
* 1495 1594: gap of unknown length
* 1595 2796: contig of 1202 bp in length

2797 2896: gap of unknown length
2897 4154: contig of 1258 bp in length
4155 4254: gap of unknown length
4255 5337: contig of 1083 bp in length
5338 5437: gap of unknown length
5438 6490: contig of 1053 bp in length
6491 6590: gap of unknown length
6591 7617: contig of 1027 bp in length
7618 7717: gap of unknown length
7718 8995: contig of 1278 bp in length
8996 9095: gap of unknown length
9096 10242: contig of 1147 bp in length
10243 10342: gap of unknown length
10343 11630: contig of 1288 bp in length
11631 11730: gap of unknown length
11731 12968: contig of 1238 bp in length
12969 13068: gap of unknown length
13069 14567: contig of 1499 bp in length
14568 14667: gap of unknown length
14668 15918: contig of 1251 bp in length
15919 16018: gap of unknown length
16019 17338: contig of 1320 bp in length
17339 17438: gap of unknown length
17439 18803: contig of 1365 bp in length
18804 18903: gap of unknown length
18904 19977: contig of 1074 bp in length
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20078 21226: contig of 1149 bp in length
21227 21326: gap of unknown length
21327 22851: contig of 1525 bp in length
22852 22951: gap of unknown length
22952 24497: contig of 1546 bp in length
24498 24597: gap of unknown length
24598 26328: contig of 1731 bp in length
26329 26428: gap of unknown length
26429 27873: contig of 1445 bp in length
27874 27973: gap of unknown length
27974 29080: contig of 1107 bp in length
29081 29180: gap of unknown length
29181 30216: contig of 1036 bp in length
30217 30316: gap of unknown length
30317 31484: contig of 1168 bp in length
31485 31584: gap of unknown length
31585 32757: contig of 1173 bp in length
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32858 34516: contig of 1659 bp in length
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34617 35905: contig of 1289 bp in length
35906 36005: gap of unknown length
36006 37093: contig of 1088 bp in length
37094 37193: gap of unknown length
37194 38553: contig of 1360 bp in length
38554 39725: gap of unknown length
39726 39825: contig of 1072 bp in length
39826 41542: gap of unknown length
41543 41642: contig of 1717 bp in length
41643 42903: gap of unknown length
42904 43003: contig of 1261 bp in length
43004 45010: gap of unknown length
45011 45110: gap of unknown length
45111 46608: contig of 1498 bp in length
46609 46708: gap of unknown length
46709 48212: gap of unknown length
48213 48312: gap of unknown length
48314 50124: contig of 1812 bp in length
50125 50224: gap of unknown length
50225 51491: contig of 1267 bp in length
51492 51591: gap of unknown length
51592 53173: contig of 1582 bp in length
53174 53273: gap of unknown length
53274 55126: contig of 1853 bp in length
55127 55226: gap of unknown length

*	55227	56787:	contlg of 1752	bp	in length
*	55679	57078:	gap of unknown	length	
*	57079	59017:	contlg of 1939	bp	in length
*	59018	59117:	gap of unknown	length	
*	59118	60347:	contlg of 1230	bp	in length
*	60348	60447:	gap of unknown	length	
*	60448	62287:	contlg of 1840	bp	in length
*	62288	62387:	gap of unknown	length	
*	62388	64079:	contlg of 1632	bp	in length
*	64080	64179:	gap of unknown	length	
*	64180	66493:	contlg of 2314	bp	in length
*	66494	66593:	gap of unknown	length	
*	66594	69033:	contlg of 2440	bp	in length
*	69034	69133:	gap of unknown	length	
*	69134	70840:	contlg of 1707	bp	in length
*	70841	70940:	gap of unknown	length	
*	70941	72857:	contlg of 1717	bp	in length
*	72658	72757:	gap of unknown	length	
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*	73541	75340:	gap of unknown	length	
*	75341	77392:	contlg of 1952	bp	in length
*	77293	77392:	gap of unknown	length	
*	77393	79809:	contlg of 1517	bp	in length
*	78910	81669:	gap of unknown	length	
*	79010	81769:	contlg of 2760	bp	in length
*	81770	84869:	gap of unknown	length	
*	84870	84966:	contlg of 2697	bp	in length
*	84967	87132:	gap of unknown	length	
*	87133	87132:	contlg of 2466	bp	in length
*	87233	89015:	contlg of 1783	bp	in length

Query Match	16.7%;	Score 65.4;	DB 2;	Length 158869
Best Local Similarity	50.8%;	Pred. No. 4.7e-06;		
Matches 120;	Conservative	0;	Mismatches 116;	Indels 0;

[illegible]

RESULT 15	
AC103331	
LOCUS	AC103331 269296 bp DNA linear HTG 13-JUL-2002
DEFINITION	Rattus norvegicus clone CH230-18711, *** SEQUENCING IN PROGRESS
ACCESSION	AC103331
VERSION	AC103331.5 GI:21731831
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus

REFERENCE
AUTHORS

1 (bases 1 to 269296)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-oshan, F.R., Allen, C.,
Alshrooks, S.L., Amartunge, H.C., Arc, J.R., Ayele, M., Banks, T.,
Barbieri, J., Benton, J., Blimge, K., Blankenburg, K., Bonini, D.,
Bouck, J., Bowle, S., Briele, M., Brown, E., Brown, M., Bryant, N.P.,
Burch, P., Burnett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	unpublished 2 (bases 1 to 269296) Morley, K.C. Direct Submission Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 269296) Morley, K.C. Direct Submission Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced gi:19111208.
REFERENCE AUTHORS TITLE JOURNAL	
COMMENT	

Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., Davis, C., Day-Carroll, L., Dederich, D. A., Delaney, K. R., Delgado, O., Dem, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Dudin, K. J., Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T. T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulik, S., Hune, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozada, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M. P., Meador, M., Mel, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newson, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokkenko, S., Oguh, M., Okwuonu, G., Oragunye, N., Oyaleto, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rotjokkan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostrat, N., Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H., Sulton, A., Swalek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansay, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wlarczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Unpublished
Direct Submission

2. (bases 1 to 269296)

Unpublished
Direct Submission

2. (bases 1 to 269296)

Worley, K.C.

Direct Submission

Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3. (bases 1 to 269296)

Worley, K.C.

Direct Submission

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2002 this sequence version replaced gi:19111208.

----- Genome Center -----

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----

Center project name: GLBP

Center clone name: CH230-18711

----- Summary Statistics -----

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 219516 bases at least Q40

Consensus quality: 221282 bases at least Q30

Consensus quality: 222447 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)

* NOTE: This is a "working draft" sequence. It currently
* consists of 49 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.

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GenCore version 5.1.4 p5.1578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 11:28:30 ; Search time 282.965 Seconds
(without alignments)
3111.799 Million cell updates/sec

Title: US-09-823-101-11

Perfect score: 391
Sequence: 1 actctcaatcacacaagacc.....taagagacgaaaaagcatgc 391

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N.Geneseq_101002:*

- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	391	100.0	391	22	AAH43645
2	63.8	16.3	6035	22	AAS39977
3	63.8	16.3	6035	22	AAK90669
4	63.8	16.3	6035	22	AAS32217
5	60.4	15.4	3773	22	AAI03116
6	60.4	15.4	3774	22	AAI03115
7	59.6	15.2	16747	22	AAI36989
8	59.6	15.2	16747	22	AAK80326
9	59.6	15.2	16747	22	AAK86604

c	10	59.6	15.2	16747	22	AAK90152	Human digestive sy
	11	59.2	15.1	670	24	ABN87790	Human ovary specif
	12	57.2	14.6	267	22	AAH43645	SSG #9. Homo sapi
	13	55.6	14.2	704	24	ABF03074	Human breast speci
	14	55.2	14.1	474	23	ABV56492	Human prostate exp
	15	54.2	13.9	382	22	AAI87526	Human polynucleoti
	16	53.4	13.7	461	24	ABR04086	Human ovary specif
	17	53.2	13.6	643	24	ABN87819	Human ovary specif
	18	53.2	13.6	845	21	AACT7730	Human cancer assoc
	19	53	13.6	451	22	AAI83042	Human polynucleoti
	20	52.8	13.5	312	23	ABV49380	Human prostate exp
	21	52.8	13.5	1016	21	AACT8044	Human cancer assoc
	22	52.6	13.5	983	24	ABN74000	Bovine embryonic g
	23	52.2	13.4	284	23	ABV49372	Human prostate exp
	24	52	13.3	303	23	ABV49738	Human prostate exp
	25	51.8	13.2	493	24	ABF03073	Human breast speci
	26	51.8	13.2	498	22	AAI88558	Human polynucleoti
	27	51.6	13.2	371	21	AAAC98006	Human colon cancer
	28	51.6	13.2	411	23	ABV19296	Human prostate exp
	29	51.4	13.1	402	22	AAI83076	Human polynucleoti
	30	51.2	13.1	320	23	ABV49152	Human prostate exp
	31	51.2	13.1	6065	22	AAV97908	Human secreted pro
	32	51.2	13.1	6066	24	ABO54960	Human ovarian antl
	33	51	13.0	1192	24	ABN87820	Human ovary specif
	34	51	13.0	1937	23	ABV23182	Human prostate exp
	35	50.8	13.0	138	21	AACT8404	Human cancer assoc
	36	50.8	13.0	422	22	AAI88931	Human polynucleoti
	37	50.8	13.0	448	22	AAI80552	Human polynucleoti
	38	50.8	13.0	2780	21	AAI26422	Human secreted pro
	39	50.6	12.9	406	22	AAI88562	Human polynucleoti
	40	50.4	12.9	214	23	ABV49510	Human prostate exp
	41	50.2	12.8	411	22	AAI84610	Human polynucleoti
	42	50.2	12.8	416	22	AAI83621	Human polynucleoti
	43	50	12.7	400	23	ABV52913	Human prostate exp
	44	49.8	12.7	287	23	ABV49457	Human prostate exp
	45	49.8	12.7	335	23	ABV49238	Human prostate exp

ALIGNMENTS

RESULT 1	AAH43645	standard; cDNA; 391 BP.
ID	AAH43645	
XX	AAH43645:	
AC	21-JAN-2002	(first entry)
DT	XX	
XX	XX	
DE	SSG #11.	
XX	XX	
KW	Stomach cancer specific gene; SSG; polymerase chain reaction; PCR;	
KW	amplify; primer; subtracted library; expressed sequence tag; EST; ss.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	W0200175169-A2.	
XX	11-OCT-2001.	
PD	XX	
XX	30-MAR-2001; 2001WO-US10591.	
PF	30-MAR-2000; 2000US-193095P.	
XX	XX	
PR	30-MAR-2000; 2000US-193095P.	
XX	XX	
PA	(DIAD-) DIADEXUS INC.	
XX	Pluta J, Chen S, Hu P, Recipon H, Macina RA;	
PI	WPI; 2001-656992/75.	
XX	XX	
DR	New Stomach Cancer Specific Genes, useful for diagnosing, monitoring,	
XX	staging, imaging or treating cancer, particularly stomach cancer	
PT	XX	
XX	XX	

PS Claim 1; Page 69; 71pp; English.

CC The sequences given in AH43636-47 represent Stomach Cancer Specific
CC Genes (SSG's). These polynucleotides were isolated using a PCR based
CC subtractive hybridization method on subtracted libraries which were
CC generated for stomach. The cDNA libraries contained expressed sequence
CC tags (EST's) from genes that are stomach cancer specific or are
CC upregulated in stomach. These polynucleotides and the corresponding
CC encoded polypeptides are useful for diagnosing, monitoring, staging,
CC imaging or treating cancer, particularly stomach cancer.

SQ Sequence 391 BP; 151 A; 81 C; 112 G; 47 T; 0 other;

Query Match	100.08;	Score 391;	DB 22;	Length 391;
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Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACTGTTCAATTCACAAAGACCTGATGCAAAAACACGAAAGGGGAGATGTGAGGGATTCAG	60
Db	1	ACTGTTCAATTCACAAAGACCTGATGCAAAAACACGAAAGGGGAGATGTGAGGGATTCAG	60
QY	61	TCAGAGTGTGGGCTCAAGAGTGACTTAATGAGGCGCTGTCTCAAGGTTCTGTAATTAAT	120
Db	61	TCAGAGTGTGGGCTCAAGAGTGACTTAATGAGGCGCTGTCTCAAGGTTCTGTAATTAAT	120
QY	121	AAACAGAGTAAAGCAAGTCATCAACAAAAAATAAAAAAAAAAAAAAAAAAAGGTTTGGGG	180
Db	121	AAACAGAGTAAAGCAAGTCATCAACAAAAAATAAAAAAAAAAAAAAAAAAAGGTTTGGGG	180
QY	181	GGGGGGCCCCCTCCCCCCCCCATTTCCGGGCGTGTTGTCCCGTGAAAAAAGGGGCCCAAT	240
Db	181	GGGGGGCCCCCTCCCCCCCCCATTTCCGGGCGTGTTGTCCCGTGAAAAAAGGGGCCCAAT	240
QY	241	ATACACTAGTTTCCCCGGGGGGAGAAAAACAATAAAACAAAAAAACGAGGGGGG	300
Db	241	ATACACTAGTTTCCCCGGGGGGAGAAAAACAATAAAACAAAAAAACGAGGGGGG	300
QY	301	GGGACCCCCGGGGGACCAACAGGGGAGCCGGGGGGAGAAAAGGGGAGACCCGGGCCAAAAA	360
Db	301	GGGACCCCCGGGGGACCAACAGGGGAGCCGGGGGGAGAAAAGGGGAGACCCGGGCCAAAAA	360
QY	361	CCCCCAAAATTAAGAGACGAAAAAGCATGC	391
Db	361	CCCCCAAAATTAAGAGACGAAAAAGCATGC	391

RESULT 2
AAS39977

AC AAS39977;

DT 17-DEC-2001 (first entry)

DE Genomic sequence #396 encoding human colon associated polypeptide.

KW Human; colon cancer; congenital abnormality; infection; colitis;
 KW Inflammatory bowel disease; IBD; neoplastic disorder; gene therapy
 KW Intestinal inflammatory disorder; malabsorption syndrome; gastric;
 KW sigmoid disease; antibacterial; antiviral; antiinflammatory;
 KW cytostatic; ds.

OS	Homo sapiens.
XX	
PN	MO200155302-a2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001MO-US01240.
XX	
PR	31-JAN-2000; 2000US-0179065.
PR	04-FEB-2000; 2000US-0180628.
PR	24-FEB-2000; 2000US-0184664.

PR	02-MAR-2000	2000US-0186350
PR	15-MAR-2000	2000US-0189674
PR	17-MAR-2000	2000US-0190076
PR	18-APR-2000	2000US-0198123
PR	19-MAY-2000	2000US-0205515
PR	07-JUN-2000	2000US-0209467
PR	28-JUN-2000	2000US-0214886
PR	30-JUN-2000	2000US-0215135
PR	07-JUL-2000	2000US-0216647
PR	07-JUL-2000	2000US-0216680
PR	11-JUL-2000	2000US-0217486
PR	11-JUL-2000	2000US-0217497
PR	14-AUG-2000	2000US-0225513
PR	14-AUG-2000	2000US-0225514
PR	14-AUG-2000	2000US-0225566
PR	14-AUG-2000	2000US-0225567
PR	14-AUG-2000	2000US-0225568
PR	14-AUG-2000	2000US-0225570
PR	14-AUG-2000	2000US-0225547
PR	14-AUG-2000	2000US-0225578
PR	14-AUG-2000	2000US-0225587
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PR	30-ANG-2000	2000US-0228924
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PR	05-SEP-2000	2000US-0229513
PR	06-SEP-2000	2000US-0230437
PR	06-SEP-2000	2000US-0230438
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PR	08-SEP-2000	2000US-0231413
PR	08-SEP-2000	2000US-0231414
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PR	29-SEP-2000	2000US-0236569
PR	02-OCT-2000	2000US-0236570
PR	02-OCT-2000	2000US-0236802
PR	02-OCT-2000	2000US-0237037
PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237039

CC	The present invention relates to the isolation of novel human colon
CC	associated polypeptides (AAU22468-AAU22701), and the cDNA and genomic
CC	sequences encoding for them. The sequences of the invention are useful
CC	in the diagnosis, treatment, prevention and/or prognosis of disorders
CC	of the colon including colon cancer, congenital abnormalities
CC	(e.g. atresia and stenosis), bacterial and viral infections,
CC	inflammatory bowel disease (IBD), neoplastic cell disorders
CC	(e.g. polyps and adenomas), intestinal inflammatory disorders, colitis,
CC	colonic inflammation, diarrhoea and dysentery, malabsorption syndromes
CC	(e.g. lactose intolerance), intestinal obstruction and sigmoid diseases.
CC	The polynucleotide sequences of the invention can also be used in gene
CC	therapy. AAS39582-AAS40060 represent DNA sequences encoding for the
CC	novel human colon associated polypeptides of the invention.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SO	Sequence 6035 BP; 1730 A; 1107 C; 1370 G; 1828 T; 0 other;
	Query Match 16.3%; Score 63.8; DB 22; Length 6035;
	Best Local Similarity 72.2%; Pred. NO. 4e-05;
	Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY	68 GGTGGGCTCAAGAGTGGACTATAGTGGGCTGTCCAAAGCTTCTGATAATAACAGA 127
Db	3535 GGCCTGCTCGAGTACGACTTATATGAGGCGTGTTCACAGGTTCTCCAAATAATAACAGA 3594
OY	128 GTAACCACTGCATCAAAAAAAAAAAAAAAAAAAAAAAAAAAGGTTGGGGCG 182
Db	3595 GTAACCAAGTCTACTAACCAATTTGATGGCTGAACAGAAAAAGTTTCTAGGGCC 3649
	RESULT 3
AAK90669	
ID	AAK90669 standard; DNA: 6035 BP.
XX	
AC	AAK90669;
XX	
DT	05-NOV-2001 (first entry)
XX	
DE	Human digestive system antigen genomic sequence SEQ ID NO: 4245.
XX	
KW	Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW	ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW	digestive system disorder; Meckel's diverticulum; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200155314-A2.
XX	
PD	02-AUG-2001.
XX	
FE	17-JAN-2001; 2001WO-US01324.
XX	
XX	
PR	31-JAN-2000; 2000US-0179065.
PR	04-FEB-2000; 2000US-0180628.
PR	24-FEB-2000; 2000US-0184664.
PR	02-MAR-2000; 2000US-0186350.
PR	16-MAR-2000; 2000US-0189874.
PR	17-MAR-2000; 2000US-0190076.
PR	18-APR-2000; 2000US-0198123.
PR	19-MAY-2000; 2000US-0205515.
PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
PR	30-JUN-2000; 2000US-0215135.
PR	07-JUL-2000; 2000US-0216647.
PR	07-JUL-2000; 2000US-0216880.
PR	11-JUL-2000; 2000US-0217487.
PR	11-JUL-2000; 2000US-0217496.
PR	14-JUL-2000; 2000US-0218299.
PR	26-JUL-2000; 2000US-0220963.
PR	26-JUL-2000; 2000US-0220964.
PR	14-AUG-2000; 2000US-0224518.

PR	14-AUG-2000	2000US-0224519
PR	14-AUG-2000	2000US-0223214
PR	14-AUG-2000	2000US-0223213
PR	14-AUG-2000	2000US-0223266
PR	14-AUG-2000	2000US-0225677
PR	14-AUG-2000	2000US-0225267
PR	14-AUG-2000	2000US-0225268
PR	14-AUG-2000	2000US-0225270
PR	14-AUG-2000	2000US-0225447
PR	14-AUG-2000	2000US-0225577
PR	14-AUG-2000	2000US-0225758
PR	14-AUG-2000	2000US-0226759
PR	14-AUG-2000	2000US-0226759
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PR	23-AUG-2000	2000US-0227182
PR	30-AUG-2000	2000US-0227924
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PR	01-SEP-2000	2000US-0229344
PR	01-SEP-2000	2000US-0229344
PR	05-SEP-2000	2000US-0229509
PR	06-SEP-2000	2000US-0230437
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PR	08-SEP-2000	2000US-0230438
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PR	08-SEP-2000	2000US-0233081
PR	12-SEP-2000	2000US-0233168
PR	14-SEP-2000	2000US-0233397
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PR	14-SEP-2000	2000US-0233400
PR	14-SEP-2000	2000US-0234401
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PR	14-SEP-2000	2000US-0233064
PR	14-SEP-2000	2000US-0233632
PR	21-SEP-2000	2000US-0234123
PR	21-SEP-2000	2000US-0234327
PR	25-SEP-2000	2000US-0234974
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PR	26-SEP-2000	2000US-0235484
PR	26-SEP-2000	2000US-0235834
PR	27-SEP-2000	2000US-0235836
PR	27-SEP-2000	2000US-0235837
PR	29-SEP-2000	2000US-0235837
PR	29-SEP-2000	2000US-0235836
PR	29-SEP-2000	2000US-0235839
PR	29-SEP-2000	2000US-0236370
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PR	02-OCT-2000	2000US-0237039
PR	13-OCT-2000	2000US-0239345
PR	13-OCT-2000	2000US-0239350
PR	20-OCT-2000	2000US-0239397
PR	20-OCT-2000	2000US-0240189
PR	20-OCT-2000	2000US-0241826
PR	01-NOV-2000	2000US-0244617
PR	08-NOV-2000	2000US-0246474
PR	08-NOV-2000	2000US-0246475
PR	08-NOV-2000	2000US-0246476
PR	08-NOV-2000	2000US-0246477

Query	83: Conservative	0: Mismatches	32: Indels	0: Gaps	0: other
68	GGTGGGCTCAAGAGTGAAGTAAATGAGGCGTCTCAAGGTTCTGTAATTAATAACAGA	127			
16.3%	Score 63.8;	DB 22;	Length 6035;		
Best Local Similarity	72.2%;	Pred. No. 4e-05;			
Matches	83: Conservative	0: Mismatches	32: Indels	0: Gaps	0: other

DB 3535 GGCCGCTCGAGAGTAGACTTAATGAGGGCTGTTCAAGTCTCGCATATAATAACAGA 3594
QY 128 GTACAGAGCTACCTACACAAAAAAGAGGTTGGGGC 182
DB 3595 GTACAGAGAGCTACCTACATATTGATGGCTGACAGAAAAAGTTCTAGGGCC 3649

RESULT 4
AAS32217
ID AAS32217 standard; DNA; 6035 BP.
XX
AC AAS32217;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human DNA repair and processing genomic DNA #3.
XX
KW DNA processing; human; mouse; rabbit; goat; horse; cat; gene therapy;
KW chicken; sheep; immunosuppressive; antirheumatic; cytosolic; cardiant; neuroprotective;
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; noctropic; antibacterial; vitucide; fungicide; cancer;
KW ophthalmological; veterinary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder; dog;
KW wound healing; skin aging; organ transplantation; tissue regeneration;
KW anti-fertility; DNA repair protein.
XX
OS Homo sapiens.
XX
PN WO200155204-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01336.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
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PR 17-NOV-2000; 2000US-0249211.

[illegible]

Db	3595	GTACAGCAGACGTCACTATACCAATATTGATGGGCTGACACAGAAAAAGTTTCTAGGGCC	3649
RESULT 5			
AL03116			
ID	AL03116	standard; DNA; 3773 BP.	
XX			
AC	AL03116;		
XX			
DT	21-NOV-2001	(first entry)	
XX			
DE	Human reproductive system related antigen DNA SEQ ID NO: 5804.		
XX			
KW	Human; reproductive system related antigen; reproductive system disorder.		
KW	cancer; gene therapy; ds.		
XX			
OS	Homo sapiens.		
XX			
PD	WO200155320-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US01339.		
XX			
PR	31-JAN-2000; 2000US-0179065.		
PR	04-FEB-2000; 2000US-0180628.		
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PR	07-JUN-2000; 2000US-0209467.		
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PR	30-JUN-2000; 2000US-0215135.		
PR	07-JUL-2000; 2000US-0216647.		
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PR	01-SEP-2000; 2000US-0229343.		
PR	01-SEP-2000; 2000US-0229344.		
PR	01-SEP-2000; 2000US-0229345.		
PR	05-SEP-2000; 2000US-0229509.		
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PR	06-SEP-2000; 2000US-0230437.		
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PR	08-SEP-2000; 2000US-0231413.		

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PR	14-SEP-2000	2000US-0233065
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PR	29-SEP-2000	2000US-0235638
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PR	02-OCT-2000	2000US-0237040

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PR	08-NOV-2000	2000US-0246476
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PR	08-NOV-2000	2000US-0246555
PR	08-NOV-2000	2000US-0246556
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PR	08-NOV-2000	2000US-0246559
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PR	08-NOV-2000	2000US-0246611
PR	08-NOV-2000	2000US-0246613
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PR	17-NOV-2000	2000US-0249209
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PR	17-NOV-2000	2000US-0249213
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PR	17-NOV-2000	2000US-0249265
PR	17-NOV-2000	2000US-0249267
PR	17-NOV-2000	2000US-0249269
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PR	01-DEC-2000	2000US-0250160
PR	01-DEC-2000	2000US-0250391
PR	05-DEC-2000	2000US-0251030
PR	05-DEC-2000	2000US-0251988
PR	05-DEC-2000	2000US-0256719
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PR	11-DEC-2000	2000US-0254097
PR	05-JAN-2001	2001US-0259678
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	Rosen CA, Barash SC, Ruben SM,	
PI	WPI: 2001-465570/50.	
XX		
DR		
XX		
PT	Isolated nucleic acid molecule e	
XX	is used in preventing, treating	
PS	Disclosure: SEQ ID NO 5803; 1297	
XX		
CC	The present invention provides t	
XX	number of human reproductive sys	

Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition -

MP1: 2001-465570/50.

Disclosure: SEQ ID NO 5803; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used

CC In the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.

XX Sequence 3774 BP; 1155 A; 847 C; 911 G; 861 T; 0 other;

Query Match 15.4%; Score 60.4; DB 22; Length 3774;

Best Local Similarity 85.9%; Pred. No. 0.00021;

Matches 67; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ACTCTTCATCAACACACCTGATGCAAAAGAGAGAGAGAGATGTGAGGATCAG 60

Db 1871 ACCTTCATCACTAATCACTGATGCAAAAGAGAGAGAGATGTAGGGATCAC 1930

QY 61 TCAGAGGTGGGCTCA 78

Db 1931 TCAGAGGTGGGAGAAAA 1948

RESULT 7

AA36989/C
ID AA36989 standard; DNA; 16747 BP.

XX AA36989;

DT 08-JAN-2002 (first entry)

DE Human musculoskeletal system related polynucleotide SEQ ID NO 3354.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

KW antiallergic; hepatotoxic; antidiabetic; antiinflammatory; antitumor;

KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;

KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;

KW neurological disease; infection; human; secreted protein;

XX musculoskeletal system; ds.

XX Homo sapiens.

XX MO200155367-A1.

PD 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01338.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205315.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214686.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

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PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.

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PR 14-SEP-2000; 2000US-0233065.

PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.

PR 25-SEP-2000; 2000US-0234997.

PR 25-SEP-2000; 2000US-0234998.

PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-0235834.

PR 27-SEP-2000; 2000US-0235835.

PR 29-SEP-2000; 2000US-0236327.

PR 29-SEP-2000; 2000US-0236367.

PR 29-SEP-2000; 2000US-0236368.

PR 29-SEP-2000; 2000US-0236369.

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PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.

PR 02-OCT-2000; 2000US-0237038.

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PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239937.

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PR 20-OCT-2000; 2000US-0241787.

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PR 20-OCT-2000; 2000US-0241809.

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PR 01-NOV-2000; 2000US-0244617.

PR 08-NOV-2000; 2000US-0246474.

PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.

PR 08-NOV-2000; 2000US-0246477.

PR 08-NOV-2000; 2000US-0246478.

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PR 08-NOV-2000; 2000US-0246524.

PR 08-NOV-2000; 2000US-0246525.

PR 08-NOV-2000; 2000US-0246526.

PR 08-NOV-2000; 2000US-0246527.

PR 08-NOV-2000; 2000US-0246528.

PR 08-NOV-2000; 2000US-0246532.

PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.

PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 03-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -

Example 2: SEQ ID NO 3354; 781pp + Sequence Listing; English.

The invention relates to novel genes (ALU34669-ALU37666) and proteins (ABR03087-ABR04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wipo at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 16747 BP; 4203 A; 3717 C; 3840 G; 3787 T; 1200 other;

Query Match 15.2%; Score 59.6; DB 22; Length 16747;
Best Local Similarity 93.9%; Pred. No. 0.00044;
Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 68 GGTGGCTCAAGAGTTCGACTTAATGAGGCTGTCTCAAGTTCTGTAATAATAACAGA 127
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QY 128 GTAAGC 133
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Db 2127 GTAAGC 2122

RESULT 8

AAK80326/c
ID AAK80326 standard; DNA; 16747 BP.

XX AAK80326;

DT 07-NOV-2001 (first entry)

XX Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:35138.

DE Human; immune: haematopoietic; immune/haematopoietic antigen; cancer;

KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO200157182-A2.

PD 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

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XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

XX 14-AUG-2000; 2000US-0225268.

XX 14-AUG-2000; 2000US-0225270.

XX 14-AUG-2000; 2000US-0225447.

XX 14-AUG-2000; 2000US-0225757.

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XX 22-AUG-2000; 2000US-0226868.

XX 22-AUG-2000; 2000US-0227182.

XX 23-AUG-2000; 2000US-0227059.

XX 30-AUG-2000; 2000US-0228924.

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XX 01-SEP-2000; 2000US-0229343.

XX 01-SEP-2000; 2000US-0229344.

XX 01-SEP-2000; 2000US-0229345.

XX 05-SEP-2000; 2000US-0229509.

XX 05-SEP-2000; 2000US-0229513.

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PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
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PR 27-SEP-2000; 2000US-0235834.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
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PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

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PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
PS Disclosure; SEQ ID NO 35138; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 16747 BP; 4203 A; 3717 C; 3840 G; 3787 T; 1200 other;
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XX
XX Query Match 15.2%; Score 59.6; DB 22; Length 16747;
XX Best Local Similarity 93.9%; Pred. No. 0.00044;
XX Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 68 GGTGGGCTCAAGACTGAGCTTAATGAGGCTGTCTCAAGCTTGTATATAATAACAGA 127
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DB 2187 GGTGGGCTCAAGAGTGCATTAAATTAGGCTGTCTCAAGGTTCTGCAAGTAATAACAGA 2128
XX
QY 128 GTAAGC 133
XX |||||||
DB 2127 GTAAGC 2122
XX
RESULT 9
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ID AAK86604 standard; DNA: 16747 BP.
XX
XX AC AAK86604;
XX
XX

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DT 07-NOV-2001 (first entry)
 XX Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:41416.
 DE
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 KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
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 PR 20-OCT-2000; 2000US-0241826.
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 PR 05-DEC-2000; 2000US-0256719.
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 PR 08-DEC-2000; 2000US-0251868.

PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure: SEQ ID NO 41416; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 16747 BP; 4203 A; 3717 C; 3840 G; 3787 T; 1200 other;
SQ
Query Match 15.2%; Score 59.6; DB 22; Length 16747;
Best Local Similarity 93.9%; Pred. No. 0.00044;
Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 68 GGTGGGCTCAAGAGTGACTTAATGAGGCTGTCTCAAGGTCTGTATAATAAACAAGA 127
DB 2187 GGTGGGCTCAAGAGTGACTTAATGAGGCTGTCTCAAGGTCTGTATAATAAACAAGA 2128
QY 128 GTAAGC 133
DB 2127 GTAAGC 2122
RESULT 10
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ID AAK90152 standard; DNA; 16747 BP.
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XX AAK90152;
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XX 05-NOV-2001 (first entry)
DT
XX
XX Human digestive system antigen genomic sequence (SEQ ID NO: 3728.
DE
XX
XX Human digestive system antigen; gene therapy; cancer; appendicitis;
KM ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KM digestive system disorder; Meckel's diverticulum; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200155314-A2.
PN
XX
XX 02-AUG-2001.
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XX 17-JAN-2001; 2001WO-US01324.
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PR 02-OCT-2000; 2000US-0236802.

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PR 17-NOV-2000; 2000US-0249246.
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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-502630/55.
DR Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases -
PT

XX
PS Disclosure; SEQ ID NO 3728; 986bp; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention.
XX
SQ Sequence 16747 BP; 4203 A; 3717 C; 3840 G; 3787 T; 1200 other;
Query Match 15.2%; Score 59.6; DB 22; Length 16747;
Best Local Similarity 93.9%; Pred. No. 0.00044;
Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 68 GTGGGCTCAAGAGTGACTTAATGAGGCTGTCTCAAGTTCTGAATTAATAACAGA 127
DB 2187 GTGGGCTCAAGAGTGACTTAATGAGGCTGTCTCAAGTTCTGAATTAATAACAGA 2128
QY 128 GTAAGC 133
DB 2127 GTAAGC 2122
RESULT 11
ABN87790
ID ABN87790 standard; cDNA; 670 BP.
AC ABN87790;
XX
XX 12-AUG-2002 (first entry)
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XX Human ovary specific nucleic acid SEQ ID NO:1.
DE
XX Human; ovary specific nucleic acid; OSNA; ovary specific protein; OSP;
KW ovary specific gene; OSg; ovarian cancer; immune response; metastasis;
KM chromosome 1; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200240535-A2.
PN
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PD 23-MAY-2002.
XX
PF 20-NOV-2001; 2001MO-US45011.
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PR 20-NOV-2000; 2000US-252061P.
PR 27-NOV-2000; 2000US-253257P.
XX
PA (DIAD-) DIADEXUS INC.
PI Salceda S, Macina RA, Recipon H, Caferkey R, Sun Y, Liu C;
XX WPI; 2002-471617/50.
DR
XX
XX New ovary specific genes and proteins, useful as a vaccine for treating
PT patients with ovarian cancer, or for diagnosing and monitoring the
PT presence and metastases of ovarian cancer in a patient -
XX
PS Claim 1; Page 149; 260pp; English.
XX
CC ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA)
CC sequences, and ABN79297 to ABN79370 represent ovary specific protein
CC (OSP) sequences from the present invention. OSNA and OSP sequences have
CC cytostatic activity, and can be used in vaccine production and gene
CC therapy. An antibody that specifically binds to an OSP can be used for
CC treating a patient with ovarian cancer, particularly for inducing an
CC immune response against the ovarian cancer cell expressing the OSNA or
CC OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring
CC the presence and metastases of ovarian cancer in a patient.
XX

QY 382 AAAAGCATG 390

1/-SEP-2002 (first entry)

DE Human prostate expression marker CDNA 56483.
XX
XX Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
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PR 13-DEC-2000; 2000US-253281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 10898; 11750pp; English.
PS
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
CC
XX
SQ Sequence 474 BP; 234 A; 34 C; 107 G; 98 T; 1 other;
XX
XX Query Match 14.1%; Score 55.2; DB 23; Length 474;
Best Local Similarity 58.5%; Pred. No. 0.0021;
Matches 96; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
XX
QY 225 AAAAAAGGGGCCCCAATATATCACTAGTCCCGGGGGGAGAAAAACAACAAAAAC 284
DB 165 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGAGAAAAACAAAAA 224
QY 285 AAAAAAAAAAGCGGGGGGAGACCCCGGGGACCAACAGGGGAGCCGGGGGAGAAAGG 344
DB 225 AAAAAAAAAAGGGGGGGGGGGGGGAGAAAAACAAAAAGGGGGGGGAGAA 284
QY 345 GACCCCGGGCCAAACCCCAAAATTAAGAGACGAGAAAAAGCA 388
DB 285 AAAAAAGGGGGGAGAAAAACAAAAACAAAAACAAAAACAA 328
XX
XX RESULT 15
AI187526
ID AA187526 standard; cDNA; 382 BP.
XX
XX AI187526;
XX

DT 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 7586.
DE
XX
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX
XX P-PSDB; AAO07595.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 1; SEQ ID NO 7586; 1399pp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pt_sequences.
CC
XX
XX Sequence 382 BP; 265 A; 18 C; 69 G; 17 T; 13 other;
XX
XX Query Match 13.9%; Score 54.2; DB 22; Length 382;
Best Local Similarity 48.1%; Pred. No. 0.0034;
Matches 137; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
XX
QY 101 CTCAGGTTCTGTATTAATAACAGAGTAAGCACTAACAACAAAAA 160
DB 42 CTAATGTTTGAATATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 101
QY 161 AAAAAAAAAAGGTTGGGGGGGGGGCCCGCCCGCCCATTCGCGGCGTGTGTCC 220
DB 102 AA 161
QY 221 CGTGAAGAAAGGGGCCCAATATATCACTAGTCCCGGGGGGAGAAACAAAAACAA 280
DB 162 AA 221
QY 281 AAAAAAAAAAGGGGGGGGGGAGACCCCGGGGACCAACAGGGGAGCCGGGGGAGAAA 340
DB 222 AAAAAAAAAAGGGGGGGGGGGGGGGGCGGNNNNAAGAGAGAGGGGGGAGAGAAA 281
QY 341 GGGGAGCCCGGCCAAACCCCAAAATTAAGAGAGCAAAA 385
DB 282 AAAAAAGAACNGNAAAAAAGGGGNNNNAAAAAAAAAAAAAAGAA 326

Mon Mar 24 08:50:05 2003

us-09-823-101-11.rng

Page 17

Search completed: March 21, 2003, 11:55:21
Job time : 342.165 secs

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OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 16:26:05 ; Search time 44.1033 Seconds
(without alignments)
2718.857 Million cell updates/sec

Title: US-09-823-101-11

Perfect score: 391
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCRTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	87.8	22.5	7218	1	US-08-232-463-14
2	48	12.3	2065	4	US-09-370-473-5
3	46	11.8	1683	4	US-09-347-803-11
4	45.6	11.7	289	4	US-09-007-005-17
5	45.6	11.7	289	4	US-09-244-796-17
6	44.2	11.3	2852	3	US-09-027-137-2
7	44.2	11.3	2852	4	US-09-344-441-2
8	43.4	11.1	3752	4	US-09-149-476-127
9	43.2	11.0	1114	4	US-09-152-060-41
10	42.8	10.9	1872	4	US-09-291-922-27
11	42.8	10.9	3410	4	US-09-020-956-110
12	42.8	10.9	3410	4	US-09-030-607-110
13	42.8	10.9	3410	4	US-09-605-785-110
14	42.8	10.9	3410	4	US-09-439-313-110
15	42.8	10.9	3410	4	US-09-352-616A-110
16	42.8	10.9	3410	4	US-09-602-877A-100
17	42.8	10.8	2407	4	US-09-232-149A-110
18	42.4	10.8	2407	4	US-09-370-807-7
19	42.4	10.8	2407	4	US-09-921-259-7
20	42.2	10.8	1206	4	US-09-465-558-53
21	42	10.7	1700	2	US-08-897-340-4
22	42	10.7	1700	3	US-09-252-329-4
23	41.8	10.7	1332	2	US-09-057-762-1
24	41.8	10.7	1332	3	US-08-326-119A-1
25	41.6	10.6	1878	4	US-09-465-558-39
26	41.6	10.6	2378	4	US-08-802-8050-20
27	41.2	10.5	599	4	US-09-342-647-19

28	40.8	10.4	519	4	US-09-227-357-76	Sequence 76, Appl
29	40.8	10.4	780	2	US-08-540-804-36	Sequence 36, Appl
30	40.8	10.4	780	4	US-08-590-399-36	Sequence 36, Appl
31	40.8	10.4	2995	4	US-09-149-476-280	Sequence 280, App
32	40.8	10.4	6671	1	US-08-280-443-1	Sequence 1, Appl1
33	40.8	10.4	6671	1	US-08-457-459-1	Sequence 1, Appl1
34	40.8	10.4	6671	1	US-08-555-678-1	Sequence 1, Appl1
35	40.8	10.4	6671	5	PCT-US95-02275-1	Sequence 1, Appl1
36	40.6	10.4	1279	3	US-09-248-335-25	Sequence 25, Appl
37	40.6	10.4	1934	4	US-08-776-844-1	Sequence 1, Appl1
38	40.6	10.4	2239	4	US-09-196-390-1	Sequence 1, Appl1
39	40.6	10.4	6755	3	US-08-931-999-4	Sequence 4, Appl1
40	40.4	10.3	688	6	5498694-3	Sequence 5, Appl1
41	40.4	10.3	1804	2	US-08-504-459-5	Sequence 1, Appl1
42	40.4	10.3	2581	4	US-09-363-708-1	Sequence 1, Appl1
43	40.4	10.3	4843	3	US-08-986-485-1	Sequence 1, Appl1
44	40.2	10.3	370	4	US-09-376-113-1	Sequence 1, Appl1
45	40.2	10.3	1210	4	US-09-443-041A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
; US-08-232-463-14
Query Match 22.5%; Score 87.8; DB 1; Length 7218;

Best Local Similarity 2.1%; Pred. No. 3.1e-13;
Matches 8; Conservative 252; Mismatches 119; Indels 0; Gaps 0;

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QY 13 ACAAGACCTGATCCAAAAACAAAAAGGGAAGATGTGAGGATCAGTCAGAGTGTGG 72
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Db 1436 ACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1377
QY 73 GCTCAGAGTGAAGTAAATGAGGCTGTCTCAGAGTTCTGTAAATAAACAAGAGTAAG 132
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1376 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1317
QY 133 CAGTCTACTAACAAAAAAGGTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 192
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1316 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1257
QY 193 CCCCCCCTCCGGCGTGTGTCCCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 252
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1256 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1197
QY 253 CCGGGGGGAGAAACAAAAAACAACAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAG 312
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1196 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1137
QY 313 GACCAACAGGGGAGCGGGGGGAGAAAGGGAGCCCGGCGCAAAACCCCGCAAAAT 372
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1136 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1077
QY 373 AAGAGAGGAAAAAGCATGC 391
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1076 RRRRRRRRRRRATGCCAAGC 1058
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RESULT 2
US-09-370-473-5
Sequence 5, Application US/09370473

```
Patent No. 6271031
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Pamodu, Layo O.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Oinolinate Metabolism Enzymes
FILE REFERENCE: BB-1209
CURRENT APPLICATION NUMBER: US/09/370,473
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/096,240
EARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 2065
TYPE: DNA
ORGANISM: Trifolium aestivum
US-09-370-473-5
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Query Match 12.3%; Score 48; DB 4; Length 2065;
Best Local Similarity 57.2%; Pred. No. 0.0021;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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QY 114 AATAAATAACAGATACAGTACTAACAACAAAAAAGG 173
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1821 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1880
QY 174 TTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 233
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1881 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1940
QY 234 CCCAATATACACTAGTCCCGGGGGGAGAA 265
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1941 CCGTTTAAAAAGTCTCGAGGGGAGAA 1972
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 3
US-09-347-803-11

Sequence 11, Application US/09347803
Patent No. 6274379

```
GENERAL INFORMATION:
APPLICANT: Pamodu, Layo O.
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
LENGTH: 1683
TYPE: DNA
ORGANISM: Oryza sativa
US-09-347-803-11
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Query Match 11.8%; Score 46; DB 4; Length 1683;
Best Local Similarity 59.0%; Pred. No. 0.0063;
Matches 79; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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QY 114 AATAAATAACAGATACAGTACTAACAACAAAAAAGG 173
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1267 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1326
QY 174 TTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 233
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1327 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1386
QY 234 CCCAATATACACT 247
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1387 GTCTTTAAAAACT 1400
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 4
US-09-007-005-17

```
Sequence 17, Application US/09007005B
Patent No. 6258558
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rih
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
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Query Match 11.7%; Score 45.6; DB 4; Length 289;
Best Local Similarity 14.2%; Pred. No. 0.0047;
Matches 40; Conservative 98; Mismatches 144; Indels 0; Gaps 0;

Db **188** SRRNRSSRNNRSRNRRNSRNRRNSRCACAGRCURGRCGRURARARCVRCR **247**

corley, Neil C.

```

1 YUE, Henry
2 TITLE OF INVENTION: CAFL-RELATED PROTEIN
3 NUMBER OF SEQUENCES: 3
4 CORRESPONDENCE ADDRESSES:
5 ADDRESS: Incyte Pharmaceuticals, Inc.
6 STREET: 3174 Porter Dr.
7 CITY: Palo Alto
8 STATE: CA
9 COUNTRY: USA
10 ZIP: 94304
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Diskette
13 COMPUTER: IBM Compatible
14 OPERATING SYSTEM: DOS
15 SOFTWARE: FASTSEQ for Windows Version 2.0
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/344,441
18 FILING DATE: 20-FEB-1998
19 CLASSIFICATION: <Unknown>
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 09/027,137
22 FILING DATE: 1998-02-20
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Billings, Lucy J.
25 REGISTRATION NUMBER: 36,749
26 REFERENCE/DOCKET NUMBER: PF-0476 US
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 650-855-0555
29 TELEFAX: 650-845-4166
30 INFORMATION FOR SEQ ID NO: 2:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 2852 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 IMMEDIATE SOURCE:
37 LIBRARY: PROSNOT16
38 CLONE: 2229466
39 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
40 US-09-344-441-2
41
42 Query Match 11.3%; Score 44.2; DB 4; Length 2852;
43 Best Local Similarity 61.9%; Pred. NO. 0.021;
44 Matches 70; Conservative 0; Mismatches 43; Indels 0; Gaps 0
45
46 Oy 262 AGAACAACAAAAACAAAAACAAAAACGGGGGGGGGACCCCGGGGACCAACAG 321
47 1 1111 111111 11111 11111111 11111 1 1111 111
48 Db 2555 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGCCCTCTAGGGGTCACAGCTT 2614
49
50 Oy 322 GGGACCGCGGGGAGAAAAAGGGGCGCCAAAAACCCCAAAATAA 374
51 1 111111 11111 11 1111 11111111 11
52 Db 2615 TAGTACGGGGGCTTGGGGGCTCAAGCCCTCTTAAGGGGCCCCCAATTTCA 2667
53
54 RESULT 8
55 US-09-149-476-127
56 Sequence 127, Application US/09149476
57 Patent No. 6420526
58 GENERAL INFORMATION:
59 APPLICANT: Rosen et al.
60 TITLE OF INVENTION: 186 Human Secreted proteins
61 FILE REFERENCE: P2002p1
62 CURRENT APPLICATION NUMBER: US/09/149,476
63 CURRENT FILING DATE: 1998-09-08
64 EARLIER APPLICATION NUMBER: PCT/US98/04493
65 EARLIER FILING DATE: 1998-03-06
66 EARLIER APPLICATION NUMBER: 60/040,162
67 EARLIER FILING DATE: 1997-03-07
68 EARLIER APPLICATION NUMBER: 60/040,333
69 EARLIER FILING DATE: 1997-03-07
70 EARLIER APPLICATION NUMBER: 60/038,621
71 EARLIER FILING DATE: 1997-03-07
72 EARLIER APPLICATION NUMBER: 60/040,626

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EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040, 334
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040, 336
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040, 163
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/047, 600
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 615
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 597
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 502
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 618
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 503
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 592
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 581
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 584
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 500
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 587
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 492
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 596
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 613
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 588
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047, 601
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 568
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 314
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 566
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 674
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 669
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 312
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 313
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043, 672
EARLIER FILING DATE:	1997-04-11

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1 EARLIER FILING DATE: 1997-04-11
2 EARLIER APPLICATION NUMBER: 60/043,576
3 EARLIER FILING DATE: 1997-04-11
4 EARLIER APPLICATION NUMBER: 60/047,501
5 EARLIER FILING DATE: 1997-05-23
6 EARLIER APPLICATION NUMBER: 60/043,670
7 EARLIER FILING DATE: 1997-04-11
8 EARLIER APPLICATION NUMBER: 60/056,632
9 EARLIER FILING DATE: 1997-08-22
10 EARLIER APPLICATION NUMBER: 60/056,664
11 EARLIER FILING DATE: 1997-08-22
12 EARLIER APPLICATION NUMBER: 60/056,876
13 EARLIER FILING DATE: 1997-08-22
14 EARLIER APPLICATION NUMBER: 60/056,881
15 EARLIER FILING DATE: 1997-08-22
16 EARLIER APPLICATION NUMBER: 60/056,909
17 EARLIER FILING DATE: 1997-08-22
18 EARLIER APPLICATION NUMBER: 60/056,875
19 EARLIER FILING DATE: 1997-08-22
20 EARLIER APPLICATION NUMBER: 60/056,862
21 EARLIER FILING DATE: 1997-08-22
22 EARLIER APPLICATION NUMBER: 60/056,887
23 EARLIER FILING DATE: 1997-08-22
24 EARLIER APPLICATION NUMBER: 60/056,908
25 EARLIER FILING DATE: 1997-08-22
26 EARLIER APPLICATION NUMBER: 60/048,964
27 EARLIER FILING DATE: 1997-06-06
28 EARLIER APPLICATION NUMBER: 60/057,650
29 EARLIER FILING DATE: 1997-09-05
30 EARLIER APPLICATION NUMBER: 60/056,884
31 EARLIER FILING DATE: 1997-08-22
32 EARLIER APPLICATION NUMBER: 60/057,669
33 EARLIER FILING DATE: 1997-09-05
34 EARLIER APPLICATION NUMBER: 60/049,610
35 EARLIER FILING DATE: 1997-06-13
36 EARLIER APPLICATION NUMBER: 60/061,060
37 EARLIER FILING DATE: 1997-10-02
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 3410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-110

Query Match 10.9%; Score 42.8; DB 4; Length 3410;
Best Local Similarity 56.6%; Pred. No. 0.05;
Matches 77; Conservative 1; Mismatches 58; Indels 0; Gaps 0;

QY 35 GAAAGGGGGAAGTGTGAGGATCAGTCAGAGTGTGGCTCAAGAGTGAATGAG 94
DB 3250 GAATATTTTAACTGTAAGTGAAGCAATGAGTAAATGTTAATGGTACAAATTAAG 3309
QY 95 GCGTGTCTCAAGTTCGTATAATAAACAAGACTAAGCAGTCACTAACAAAAAAA 154
DB 3310 GCTTCTTATATGTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAR 3369
QY 155 AAAAAAAAAAAAAA 170
DB 3370 AAAAAAAAAAAAAA 3385

RESULT 13

US-09-605-785-110
Sequence 110, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 110
LENGTH: 3410
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-110

Query Match 10.9%; Score 42.8; DB 4; Length 3410;
Best Local Similarity 56.6%; Pred. No. 0.05;
Matches 77; Conservative 1; Mismatches 58; Indels 0; Gaps 0;

QY 35 GAAAGGGGGAAGTGTGAGGATCAGTCAGAGTGTGGCTCAAGAGTGAATGAG 94
DB 3250 GAATATTTTAACTGTAAGTGAAGCAATGAGTAAATGTTAATGGTACAAATTAAG 3309
QY 95 GCGTGTCTCAAGTTCGTATAATAAACAAGACTAAGCAGTCACTAACAAAAAAA 154
DB 3310 GCTTCTTATATGTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAR 3369
QY 155 AAAAAAAAAAAAAA 170
DB 3370 AAAAAAAAAAAAAA 3385

RESULT 14

US-09-439-313-110
Sequence 110, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Renger, Gary
APPLICANT: Retter, Marc
APPLICANT: Stolk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 110
LENGTH: 3410
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-110

Query Match 10.9%; Score 42.8; DB 4; Length 3410;
Best Local Similarity 56.6%; Pred. No. 0.05;
Matches 77; Conservative 1; Mismatches 58; Indels 0; Gaps 0;

QY 35 GAAAGGGGGAAGTGTGAGGATCAGTCAGAGTGTGGCTCAAGAGTGAATGAG 94
DB 3250 GAATATTTTAACTGTAAGTGAAGCAATGAGTAAATGTTAATGGTACAAATTAAG 3309
QY 95 GCGTGTCTCAAGTTCGTATAATAAACAAGACTAAGCAGTCACTAACAAAAAAA 154
DB 3310 GCTTCTTATATGTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAR 3369
QY 155 AAAAAAAAAAAAAA 170
DB 3370 AAAAAAAAAAAAAA 3385

RESULT 15

US-09-352-616A-110
Sequence 110, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun

```

; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; SOFTWARE: FASTSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-352-616A-110

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Query Match      10.9%; Score 42.8; DB 4; Length 3410;
Best Local Similarity 56.6%; Pred. No. 0.05;
Matches 77; Conservative 1; Mismatches 58; Indels 0; Gaps 0;

QY 35 GAAAGGGGAGATGTGAGGATCACTGAGTGGGCTCAAGAGTGAGCTTAATGAG 94
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3250 GAATATTTTATCTAGTGAAGCAATCAAGATATATGTTTATGTTGACCAATTAAG 3309
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QY 95 GGCTGTCTCAGCTTCTGTATATAATAACAGAGTAAGCAGTCACTAACAAAAAAA 154
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DB 3310 GCTTCTTATATGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAR 3369
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QY 155 AAAAAAAAAAAAAAA 170
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DB 3370 AAAAAAAAAAAAAAA 3385
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Search completed: March 21, 2003, 19:17:27
 Job time : 72.1033 secs


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Db 181 GCGGGGCCCCCTCCCGGCGTGTGTCTCCCGTGAAGAGGGCCCAAT 240
Qy 241 ATACACTAGTTCCTCCGGGGGAGAAAAACAAAAACAAAAACGGGGGG 300
Db 241 ATACACTAGTTCCTCCGGGGGAGAAAAACAAAAACAAAAACGGGGGG 300
Qy 301 GGGACCCCGGGGAGCAACAGGGAGCCGGGGGAGAAAGGGAGCCCGGCCA 360
Db 301 GGGACCCCGGGGAGCAACAGGGAGCCGGGGGAGAAAGGGAGCCCGGCCA 360
Qy 361 CCCCCCAAAATATAGAGAGCAAAAGCATGC 391
Db 361 CCCCCCAAAATATAGAGAGCAAAAGCATGC 391
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RESULT 2

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US-09-764-872-874
; Sequence 874, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 874
; LENGTH: 6035
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-872-874
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Query Match 16.3%; Score 63.8; DB 9; Length 6035;
Best Local Similarity 72.2%; Pred. No. 0.00017;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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Qy 68 GGTGGGCTCAAGAGTGAAGGCTGTCTCAAGGTTCTGAATTAATTAACAGA 127
Db 3535 GCGCGGCTCGAGAGTAGACTTAATGAAGGCTGTTTCAGGTTCTGCAATTAATTAACAGA 3594
Qy 128 GTAAGCAGTCACTAACAAAAAAGGTTGGGGGC 182
Db 3595 GTAAGCAGTCACTAACAAATTGATGGCTGACAGAAAAAGTTCTGAGGCC 3649
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RESULT 3

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US-10-078-090-102
; Sequence 102, Application US/10078090
; Publication No. US20030044815A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Kaira, Kalpana
; APPLICANT: Caffierkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PR
; FILE REFERENCE: DEX-0312
; CURRENT APPLICATION NUMBER: US/10/078,090
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/268,999
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapien
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US-10-078-090-102

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Query Match 15.6%; Score 61; DB 9; Length 447;
Best Local Similarity 68.0%; Pred. No. 0.0004;
Matches 100; Conservative 0; Mismatches 45; Indels 2; Gaps 1;
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Qy 231 GGGCCCAATATACACTAGTTCCTCCGGGGGAGAAAAACAAAAACAAAAA 290
Db 301 GGGGCAACAGAGGAGCACTCTTCACAGGAAAAAAGAAAAAAGAAAAA 360
Qy 291 AACGGGGGGGGAGACCCCGGGGAGCCACACA--GGGAGCCGGGGGAGAAAGGGAGCC 348
Db 361 AGCGGGGGGGGGAACACAGAGGGGCCCAAAACGCGGGAGCCCGGGGGGGAATGCGGGAAC 420
Qy 349 CCGGGCCAAAACCCCAAAATTAAG 375
Db 421 CCGGGAGCACCAAAATTCACAAACAAAG 447
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RESULT 4

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US-09-764-877-3354/C
; Sequence 3354, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3354
; LENGTH: 16747
; TYPE: DNA
; ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: SITE
LOCATION: (14037)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14038)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14039)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14040)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14041)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14042)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14043)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14044)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14045)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14046)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14047)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (14048)
OTHER INFORMATION: n equals a,t,g, or c
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Db 404 GCGCGGGTCCCGGGGGAGAAATGGGTTCGCCGCCCAAAATTCGCCCAAAAAAGC 463
 OY 377 GACGAAAAA 385
 Db 464 GGAGAACAA 472

RESULT 8
 US-10-001-835-105
 ; Sequence 105, Application US/10001835
 ; Patent No. US20020160387A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Salceda, Susana
 ; APPLICANT: Macina, Roberto
 ; APPLICANT: Recipon, Hervé
 ; APPLICANT: Cafkerkey, Robert
 ; APPLICANT: Sun, Yongming
 ; APPLICANT: Liu, Chenghua
 ; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prc
 ; FILE REFERENCE: DEX-0277
 ; CURRENT APPLICATION NUMBER: US/10/001,835
 ; PRIOR FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/249,997
 ; NUMBER OF SEQ ID NOS: 228
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 105
 ; LENGTH: 461
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-001-835-105

Query Match 13.7%; Score 53.4; DB 9; Length 461;
 Best Local Similarity 60.8%; Pred. No. 0.015;
 Matches 87; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

OY 228 AAGGGGCCCAATATACACTAGTTCGCCGCCGGGAGAAACAAACAAACAAACAA 287
 Db 319 AATGTCATTAAGTCATTAAGTCATTAAGTCATTAAGTCATTAAGTCATTAAGTC 378
 OY 288 AAAAAGCGGGGGGGGAGACCCCGGGGACCAACAGGGAGCCGGGAGAGAAAGGGGAC 347
 Db 379 AAAAAAGGTGGGGGTAAACAAATGGGAAAAAAGGGGACCCGTGTTGAAAAATTAATTAC 438
 OY 348 CCGGGGCCAAACCCGCCAAA 370
 Db 439 CCCAGACAAAAATTCACGCAA 461

RESULT 9
 US-09-925-301-124
 ; Sequence 124, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 124
 ; LENGTH: 845
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (823)
 ; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature
 ; LOCATION: (825)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-925-301-124

Query Match 13.6%; Score 53.2; DB 10; Length 845;
 Best Local Similarity 70.0%; Pred. No. 0.018;
 Matches 70; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 98 TGTCTCAAGTTCTGTAATAATTAACAGAGTAAGCAGTCACTACACAAAAA 157
 Db 746 TGGCGCTACAAACACTAAAAA 805
 OY 158 AAAAAAAGGTTGG 197
 Db 806 AAAAAAATTTGG 845

RESULT 10
 US-09-925-301-438
 ; Sequence 438, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 438
 ; LENGTH: 1016
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (27)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (993)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (994)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (995)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-925-301-438

Query Match 13.5%; Score 52.8; DB 10; Length 1016;
 Best Local Similarity 72.5%; Pred. No. 0.022;
 Matches 66; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 108 TTCTGTAATAATTAACAGAGTAAGCAGTCACTACACAAAAA 167
 Db 925 TTCTGTAATAATTAACAGAGTAAGCAGTCACTACACAAAAA 984
 OY 168 AAGGCTTTGG 198
 Db 985 AAAAAAATTTGG 1015

RESULT 11
 US-10-001-887-78
 ; Sequence 78, Application US/10001887
 ; Patent No. US20020155464A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Salceda, Susana
 ; APPLICANT: Macina, Roberto

```

; APPLICANT: Recipon, Hervé
; APPLICANT: Caffery, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0269
; CURRENT APPLICATION NUMBER: US/10/001,887
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,998
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/252,563
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (264)..(264)
; OTHER INFORMATION: a, c, g or t
; NAME/KEY: misc_feature
; LOCATION: (250)..(250)
; OTHER INFORMATION: a, c, g or t
; NAME/KEY: misc_feature
; LOCATION: (308)..(308)
; OTHER INFORMATION: a, c, g or t
; NAME/KEY: misc_feature
; LOCATION: (311)..(312)
; OTHER INFORMATION: a, c, g or t
; US-10-001-887-78

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Query Match      13.2%; Score 51.8; DB 9; Length 493;
Best Local Similarity 66.7%; Pred. No. 0.031;
Matches 74; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

```

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QY 260 GGAGAAACAAAAAACAACAAAAAAGGGGGGGGACCCCGGGGACCAAC 319
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 317 GAACCAAAAAAACAACAAAAAAGGGGGGGTAATCTGCGGCGCTAAG 376
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 320 AGGGAGCGGGGGGAGAAAGGGGACCCCGGGCCCAAAACCCCAAAA 370
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 377 GCGGGTTCCCGGGGGGGAATTGGTTTCCCGCCGCCACAAATTTCCCA 427
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 12
US-09-925-299-16
; Sequence 16, Application US/09925299
; General Information:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (350)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (360)
; OTHER INFORMATION: n equals a,t,g, or c

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US-09-925-299-16

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Query Match      13.2%; Score 51.6; DB 9; Length 371;
Best Local Similarity 75.0%; Pred. No. 0.033;
Matches 63; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

```

QY 114 AATAATTAACAGAGTACGACTACTAACAAAAAAGGG 173
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 288 AAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 347
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 174 TTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 197
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 348 TTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 371
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 13
US-09-925-299-16
; Sequence 16, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (350)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (360)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-16

```

```

Query Match      13.2%; Score 51.6; DB 10; Length 371;
Best Local Similarity 75.0%; Pred. No. 0.033;
Matches 63; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

```

QY 114 AATAATTAACAGAGTACGACTACTAACAAAAAAGGG 173
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 288 AAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 347
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 174 TTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 197
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 348 TTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 371
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 14
US-09-800-729-35
; Sequence 35, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P204AP1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0

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SEQ ID NO 35
LENGTH: 6065
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (6035)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (6037)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (6038)
OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-35

Query Match 13.1%; Score 51.2; DB 10; Length 6065;
Best Local Similarity 66.4%; Pred. No. 0.067;
Matches 71; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 99 GTCACAGCTCTGTAATAATACAGAGTACGACGTCTACCAAAAAAAAAAAAAA 158
DB 5936 GTTGAAGATCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5995

QY 159 AAAAAAAAAAGGTTGGGGCGGGCCCTCCCTCCCAATTC 205
DB 5996 AAAAAAAAAAACCCCGGGGGGGCCCCCCCCCNGNCC 6042

RESULT 15

US-09-925-301-798
Sequence 798, Application US/09925301
Patent No. US2002052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 798
LENGTH: 138
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (115)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (120)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (127)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (128)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (133)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-798

Query Match

13.0%; Score 50.8; DB 10; Length 138;
Best Local Similarity 65.4%; Pred. No. 0.04;
Matches 70; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 91 TGAGGGCTGTCTCAAGTCTGTAATAATACAGAGTACGACGTCTACCAAAAAA 150
DB 5996 AAAAAAAAAAACCCCGGGGGGGCCCCCCCCCNGNCC 6042

DB 32 TGTGACTGCATGATGACCTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 91

QY 151 AAAAAAAAAAAAAAAAAAGGTTGGGGCGGGCCCTCCCTCC 197

DB 92 AAAAAAAAAAAAAAAAAANCCCGGGGGGGCCCCCNGNCC 138

Search completed: March 22, 2003, 00:21:57
Job time: 102.574 secs

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Db	653	KGGAGGTTAATTTTTTMAARMGKRRTTAAAMAAAAAMATTATTRAMAAAAATRA	594
QY	148	AAAAAAAAAAAAAAAAAAAAAGGTTTGGGGGGGGGGCCCCCTCCGCCCATTCGG	207
Db	593	AAAAAAAAAAAAAAAAAAAAATGATGNNNGAGMAMNNMMQMTTGNNGNGNGG	534
QY	208	GCCTGTCTGTCCTCCCTGAAAAAGGGGCCCAATATACACTAGTTCCTCCGGGGGAGAAA	267
Db	533	GGGCTGTGNNNNMAMMMNNNNNNNNMTKTKTNNNNNNMAMMMMYNTNNNNNNMM	474
QY	268	CAAAAAAACAAAAAACAAAAAACGGGGGGGGAGCCCGGAGCACAGAGGAGC	327
Db	473	NNAAGVNNNGNNNGNNMAMMMNNNNMMGSGTGTGNCANNNMAMVEGMMNNNNNNMM	414
QY	328	CGGGGGGAGAAAGGGGAGCCCGGGCCAA	358
Db	413	MGNNNNNNMMGMMNGGGGAGGGGGGVM	383
RESULT 4			
LOCUS	BM15461		
DEFINITION	OP20536 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.		
ACCESSION	BM15461		
VERSION	BM15461.1		
KEYWORDS	EST.		
SOURCE	Globodera pallida.		
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.		
REFERENCE	1 (bases 1 to 986)		
AUTHORS	Heer, J., Sosninski, B., Pokrzywa, R. M., Watry, A. and Opperman, C.		
JOURNAL	Mixed Stage EST's from Globodera pallida, the potato cyst nematode Unpublished (2001)		
COMMENT	Contact: Opperman, C Center for the Biology of Nematode Parasitism NC State University; IACR-Rothamsted Campus Box 7616; Raleigh, NC 27695, USA Tel: 919.515.6699 Fax: 919.515.9500 Email: warthog@unity.ncsu.edu Grl1-4PCN.F.E09.PCN.4.F.067.ab1.		
FEATURES			
Source	Location/Qualifiers		
	1..986		
	/organism="Globodera pallida"		
	/db_xref="taxon:36090"		
	/clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"		
	/note="Vector: lambda GT11. This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."		
BASE COUNT	251 a 364 c 35 g 282 t 54 others		
ORIGIN			
Query Match	17.1%, Score 67; DB 13; Length 986;		
Best Local Similarity	60.9%; Pred. No. 0.4;		
Matches 109; Conservative	0; Mismatches 70; Indels 0; Gaps 0;		
QY	114	AATAATTAACGACTAGCACTACTAACAAAAA	173
Db	85	AAATTT	144
QY	174	TTTGGGGCGGGCCCCCTCCGCCCATTTCCGGGCGTGTGTCCTCCGTAAGAAAGGG	233
Db	145	TTTTTGGCCCCCCCCCCCCCCCCCTGTGAGTCTACTGCATCTATTAATAA	204
QY	234	CCCAATATATACACTAGTTCCCGGGGGGAGAAAAA	292

[illegible]

[illegible]

QY	312	GGACCAACAGGGGAGCCGGGAGGAGAAAGGGGAGCCGGGAGCCCAAAACCCCAAA	371
Db	595	RRRAGRRRRRRRAAGAGARGRRRRGRARRARRAARGARRRRRRRRRRRAARRGAGCA	536
QY	372	TAAGAGACGAAAGCA	388
Db	535	CARARGRAGRRARRRA	519
RESULT 7			
LOCUS	B0777970/c	491 bp	linear EST 26-JUL-2002
DEFINITION	1139d04.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6032310 5'		
ACCESSION	B0777970		
VERSION	B0777970.1	GI:21986442	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	EmuraYotla, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Keastner,K., Lentshka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.		
TITLE	Endocrine Pancreas Consortium		
JOURNAL	Unpublished (2000)		
COMMENT	Other. ESTs: 1139d04.x1 Contact: Douglas Melton, Klaus H. Keastner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@hmp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco.		
FEATURES	Location/Qualifiers		
Source	1..491 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6032310" /clone_lib="HR85 islet" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@im.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."		
BASE COUNT	140 a 133 c 77 g 141 t		
ORIGIN			
Query Match	16.3%	Score 63.8:	DB 14: Length 491:
Best Local Similarity	72.2%	Prod. NO. 1.8:	
Matches 83: Conservative	0: Mismatches 32: Indels	0: Gaps	0:
QY	68	GGTGGCTCAAGAGGAGCTAATGAGGCGCTGTCACAGGTTCTGTATTAATAACAGA	127
Db	140	GGCGGCTCGAGAGTAACTAATGAGGCGCTGTTCAAGGTTTCATTAATAACAGA	81

QY 128 GTAGAGTCACTAACAAAAAAGGTTGGGGC 182
 Db 80 GTAGAGTCACTAACATATTTGATGGGCTGACAGAAAAAGTTCTAGGGCC 26

RESULT 8
 LOCUS Bf160057
 DEFINITION Bf160057 732 bp mRNA linear EST 30-OCT-2000
 60176774F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3984035 5',
 mRNA sequence.
 ACCESSION Bf160057
 VERSION Bf160057.1 GI:11040164
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 732)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 plate: L1AM9185 row: 9 column: 12
 High quality sequence stop: 294.

FEATURES

Source
 Location/Qualifiers
 1..732
 /organism="Mus musculus"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone_1ib="IMAGE:3984035"
 /clone_1ib="NCI_CGAP_Lu29"
 /tissue_type="spontaneous tumor, metastatic to mammary.
 Stem cell origin."
 /lab_host="DH10B"
 /note="Organ: Lung; Vector: PCMV-SPORT6; Site_1: Salt;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 BASE COUNT 278 a 199 c 177 g 78 t
 ORIGIN

Query Match 16.2%; Score 63.4; DB 12; Length 732;
 Best Local Similarity 53.4%; Pred. No.1.6; Indels 0; Gaps 0;
 Matches 133; Conservative 0; Mismatches 116;

QY 114 AATAAATTAACAGAGTAAGCACTAACAAAAAAGGTTGGGGC 173
 Db 223 AAAAAAATTAACAGAGTAAGCACTAACAAAAAAGGTTGGGGC 282
 QY 174 TTGG 233
 Db 283 AAAGAGAGGG 342
 QY 234 CCCCAATATACACTAGTTCCCGGGGAGAAAAAACAATAAACAATAAACA 293
 Db 343 CCCCAATATACAGAGTAAGCACTAACAAAAAAGGTTGGGGC 402
 QY 294 GGG 353
 Db 403 AGCAGCGGG 462
 QY 354 CCAAAAAACC 362
 Db 463 CGAACCCAC 471

RESULT 9
 LOCUS CNS014HQ/c 983 bp DNA linear GSS 26-JUL-1999
 DEFINITION BACN11P03 of Drosophila genome survey sequence 17 end of BAC
 fly), genomic survey sequence.
 ACCESSION AL104168.1 GI:5615779
 VERSION AL104168.1
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 983)
 Direct Submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billard at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.

FEATURES

Source
 Location/Qualifiers
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 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_1ib="BACN11P03"
 /clone_1ib="DrosBAC"
 /plasmid="pBelobAC11"
 /note="end : 17"
 BASE COUNT 67 a 157 c 126 g 259 t 374 others
 ORIGIN

Query Match 16.0%; Score 62.6; DB 17; Length 983;
 Best Local Similarity 27.2%; Pred. No.1.7;
 Matches 101; Conservative 109; Mismatches 162; Indels 0; Gaps 0;

QY 12 AACAGACCTGATCAAAAAACAGAAAGGGAAGTGTGAGGATCACTAGTGTGTG 71
 Db 875 AAAAAARRKDDAADAADAADAAKGGKGGKGAAGGKGAAGAGKAGKGA 816
 QY 72 GGCTCAAGAGTGAATGAGGGCTGTCTCAAGGTTCTGTAATAAATTAACAGAGTAA 131
 Db 815 KAAAKKRDADAAAAAAGGAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 756
 QY 132 GCACACTAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 191
 Db 755 KDKRAAKHKKDAKKAAGGKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 696
 QY 192 TCCCGGG 251
 Db 695 CCCCCCCCCCMKVMKAVDVKMKCRKKCKMKACGKKKVMKMMKMMKAAVMM 636
 QY 252 CCGGGGGGGGAGAAACAAAAAACAATAAATAAATAAATAAATAAATAAATAAATA 311
 Db 635 MAMMMAMMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMM 576
 QY 312 GGACCAACAGGGGAGCGGGGGGAGAAAGGGGAGCCCGGGCCAAATATACACTGTT 371
 Db 575 KAKSKARKAAAAAGKKNCKMMAAADAARDDMAAGKCCCAADKCAMGAARAAA 516
 QY 372 TAAGAGACGAAA 383
 Db 515 AMACACCMARA 504

```

RESULT 10
LOCUS      AU234861                      850 bp    mRNA    linear    EST 26-OCT-2001
DEFINITION AU234861 Amphioxus Notochord cDNA library Branchiostoma belcheri
ACCESSION  AU234861
VERSION     AU234861.1 GI:16501008
KEYWORDS    EST.
SOURCE      Branchiostoma belcheri.
            Branchiostoma belcheri.
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1 (bases 1 to 850)
AUTHORS     Suzuki,M.M. and Satoh,N.
TITLE       Genes expressed in the amphioxus notochord revealed by EST analysis
JOURNAL     Dev. Biol. 224 (2), 168-177 (2000)
MEDLINE     20387132
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@es.cidlan.zool.kyoto-u.ac.jp.
FEATURES
    source      1..850
                /organism="Branchiostoma belcheri"
                /db_xref="taxon:7741"
                /clone="Bb3.01609"
                /clone_11b="Amphioxus Notochord cDNA library"
                /tissue_type="notochord"
BASE COUNT   282 a      15 c      175 g      135 t      203 others
ORIGIN
Query Match 15.8%; Score 61.6; DB 9; Length 850;
Best Local Similarity 39.7%; Pred. No. 2.6; Indels 0; Gaps 0;
Matches 142; Conservative 0; Mismatches 216;
QY 29 AAAACGAAAGAGGGAAGTGTAGAGTCACTAGTGTGGTGGCTCAAGACTGACCTT 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTANTTGGANNNGGNGG 172
QY 89 AATGAGGCTGTCTCAAGTTCTGTAATTAATTAACAGAGTACAGTCACTAACAAAA 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 173 AAAAAAAAAATTTTNNNTGGANNNGGNNGNNAAAAAAAAAAAAAAAAAAAAA 232
QY 149 AAAAAAAAAAAAAAAAAAAGGTTTGGGGGGGGGGGGGGGGGGGGGGGGGGGG 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 233 AAAAAAAAAAAAAAAAAAANNTTTNTANAAAAAGGGGNNNNTNNNAAAAAANA 292
QY 209 CGTGTCTGTCCCGTGAAGAGGGGCCCAATATACACTAGTTCCCGGGGGGAGAAAC 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 293 ANGNNNNANCCGGGGGCTNGSAAAAAANGGNNGGAAAAAAGGGGGGGGGGG 352
QY 269 AAAAAACAAAAAACAAAAAAGCGGGGGGAGACCCCGGGGACCAACAGGGAGCC 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 353 NCGAATAAANANANANAAAAAAGGGGCGNTTGGGGCCCGGNNCCNNNGGNCN 412
QY 329 GGGGGGAGCAAGGGGAGCCCGGGGCAAAACCCCAAAATAAGAGCAAGAAAG 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 413 TTGGGTNAAAAAAGGGGNCNNNNGGNNAAAAAAGGGGGGGGGGGGGGGGG 470

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ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
AUTHORS     Genoscope.
TITLE       Direct Submision
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osogawa and
            Aaron Mamoser in Pletier de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPc1-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            pl and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES
    source      1..1101
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone="BACR22M14"
                /clone_11b="RPc1-98"
                /note="end : 17"
BASE COUNT   180 a      304 c      71 g      359 t      187 others
ORIGIN
Query Match 15.8%; Score 61.6; DB 17; Length 1101;
Best Local Similarity 34.2%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 124; Conservative 64; Mismatches 175;
QY 22 GATGCAAAAAACGAAAGGGGAGATGTGAGGATCACTAGTGTGGCTCAAGAG 81
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 967 GACAGAGANNAGRGRRAGAGGAGGAGRRRAAGGAGAGAGAGAGGGGGGRRGG 908
QY 82 TGGACTTAATGAGCGCTGTCTCAAGTTCTGTAATTAATTAACAGAGTACGACTCA 141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 907 GGAAGAAGARAGAGCGGGGARGRGAGAGAAAGAGAGAGAGARAAAGARAGARR 848
QY 142 ACAAAAAAAAAAAAAAAAAAAGGTTTGGGGGGGGGGGGGGGGGGGGGGGGGG 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 847 AGAAAGARAGAAAGARAGAAARAGARAGARAGARAGARAGARAGARAGARR 788
QY 202 TTCCGGGCGTGTCTCCCGTGAAGAGGGGCCCAATATACACTAGTTCCCGGGGGG 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 787 AARNAGRAGRGARRARAAGARAGARRRRRRGGAGAGGRRACRAGRRGR 728
QY 262 AGAAAAACAAAAAACAAAAAAGCGGGGGGAGACCCCGGGGACCAACAG 321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 727 ARARAGCAAGGRAAAGRAAARAARAARRRAGARAGAGAAGAGRAGGRRAGA 668
QY 322 GGGAGCGGGGGGAGAAAGGGGAGCCCGGGGCAAAACCCCAAAATAAGAGACGA 381
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 667 AGRGAARGGRRAGRRARAGGRRAGGAGRAGAAAGAGRAARAGAAAGAGAA 608
QY 382 AAA 384
DB 607 GAR 605

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RESULT 12
LOCUS      BM415463                      850 bp    mRNA    linear    EST 28-JAN-2002
DEFINITION BM415463 Op20538 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.

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REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 1117)	Heer, J., Sosinski, B., Pokrzywa, R. M., Wary, A. and Opperman, C.	Mixed Stage ESR's from <i>Globochloa pallida</i> , the potato cyst nematode	unpublished (2001)

Query Match 8.58; Score 54; DB 6; Length 1466

	/organism="unknown"			
BASE COUNT	521 a	209 c	299 g	443 t
ORIGIN				

Query Match 8.5%; Score 54; DB 6; Length 1472;
 Best Local Similarity 62.7%; Pred. No. 0.00087;
 Matches 84; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTGGCCCTTAACC 60
 |||||
 Db 1460 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTAAATTTAAAAA 1401
 |||||

QY 61 CTGGGCGCTTTAAATAATGGAAGCCTGAAAGTCACGCGGGGAGGAAAAACCAA 120
 |||||
 Db 1400 CAAGGGCAAAATAGTATACAAATACAGTAACATAGTAACAAAAAGCCTAA 1341
 |||||

QY 121 AAAACAGATAAAA 134
 |||||

Db 1340 GCTAACGGAATAAA 1327

RESULT 8
 AR174966 1472 bp DNA linear PAT 17-DEC-2001
 LOCUS AR174966
 DEFINITION Sequence 12 from patent US 6309644.
 ACCESSION AR174966
 VERSION AR174966.1 GI:17916265
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1472)
 AUTHORS Chandrasekar, R. and Mehta, K.
 TITLE Parasitic nematode transglutaminase proteins and uses thereof
 JOURNAL Patent: US 6309644-A 12 30-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..1472
 BASE COUNT 444 a 298 c 209 g 521 t
 ORIGIN

Query Match 8.5%; Score 54; DB 6; Length 1472;
 Best Local Similarity 62.7%; Pred. No. 0.00087;
 Matches 84; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTGGCCCTTAACC 60
 |||||
 Db 13 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTAAATTTAAAAA 72
 |||||

QY 61 CTGGGCGCTTTAAATAATGGAAGCCTGAAAGTCACGCGGGGAGGAAAAACCAA 120
 |||||
 Db 73 CAAGGGCAAAATAGTATACAAATACAGTAACATAGTAACAAAAAGCCTAA 132
 |||||

QY 121 AAAACAGATAAAA 134
 |||||

Db 133 GCTAACGGAATAAA 146

RESULT 9
 AR208551/c 1875 bp DNA linear PAT 20-JUN-2002
 LOCUS AR208551
 DEFINITION Sequence 46 from patent US 6383774.
 ACCESSION AR208551
 VERSION AR208551.1 GI:21509734
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1875)
 AUTHORS Chandrasekar, R.
 TITLE Parasitic nematode transglutaminase, nucleic acid molecules and uses thereof
 JOURNAL Patent: US 6383774-A 46 07-MAY-2002;
 FEATURES Location/Qualifiers
 source 1..1875
 /organism="unknown"

BASE COUNT 648 a 271 c 398 g 558 t
 ORIGIN

Query Match 8.5%; Score 54; DB 6; Length 1875;
 Best Local Similarity 62.7%; Pred. No. 0.0009;
 Matches 84; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTGGCCCTTAACC 60
 |||||
 Db 1863 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTAAATTTAAAAA 1804
 |||||

QY 61 CTGGGCGCTTTAAATAATGGAAGCCTGAAAGTCACGCGGGGAGGAAAAACCAA 120
 |||||
 Db 1803 CAAGGGCAAAATAGTATACAAATACAGTAACATAGTAACAAAAAGCCTAA 1744
 |||||

QY 121 AAAACAGATAAAA 134
 |||||

Db 1743 GCTAACGGAATAAA 1730

RESULT 10
 AR208552 1875 bp DNA linear PAT 20-JUN-2002
 LOCUS AR208552
 DEFINITION Sequence 48 from patent US 6383774.
 ACCESSION AR208552
 VERSION AR208552.1 GI:21509735
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1875)
 AUTHORS Chandrasekar, R.
 TITLE Parasitic nematode transglutaminase, nucleic acid molecules and uses thereof
 JOURNAL Patent: US 6383774-A 48 07-MAY-2002;
 FEATURES Location/Qualifiers
 source 1..1875
 /organism="unknown"

BASE COUNT 558 a 398 c 271 g 648 t
 ORIGIN

Query Match 8.5%; Score 54; DB 6; Length 1875;
 Best Local Similarity 62.7%; Pred. No. 0.0009;
 Matches 84; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTGGCCCTTAACC 60
 |||||
 Db 13 TTTTCTTTTCTTTTCTTTTCTTTTCCAAACAAATTTTAAATTTAAAAA 72
 |||||

QY 61 CTGGGCGCTTTAAATAATGGAAGCCTGAAAGTCACGCGGGGAGGAAAAACCAA 120
 |||||
 Db 73 CAAGGGCAAAATAGTATACAAATACAGTAACATAGTAACAAAAAGCCTAA 132
 |||||

QY 121 AAAACAGATAAAA 134
 |||||

Db 133 GCTAACGGAATAAA 146

RESULT 11
 AF008300/c 1881 bp mRNA linear INV 30-SEP-1999
 LOCUS AF008300
 DEFINITION Dirofilaria immitis transglutaminase precursor (nd1ng) mRNA, complete cds.
 ACCESSION AF008300
 VERSION AF008300.1 GI:3273481
 KEYWORDS
 SOURCE Dirofilaria immitis.
 ORGANISM Dirofilaria immitis.
 REFERENCE 1 (bases 1 to 1881)
 AUTHORS Chandrasekar, R., Tsuji, N., Morales, T., Ozols, V. and Mehta, K.
 TITLE An Erp60-like protein from the filarial parasite Dirofilaria

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Db	662	C-----AGGGTGAAGTCCACACACATGGTCTCATGCCCATATGAGTTGCACACCAAAACACA	628
QY	241	CGGGCGGCGGCGTACTCCCGCGGTGACATAAGTTCGTGGAATCTTGCAGACTTGGGTGT	300
Db	627	GGCTCTGACTTCTCCCTCCGACACTAGTCAAGTCAACTTGCAGACAT-----AGGGT	578
QY	301	ACCCCTCCCTTATATGTTTATTTCTTTTCCCGCCCTCAAAATGGGCTGGTCTTTCGCCA	360
Db	577	AACCTCACAATATCACTATTAATCTTTTCCACACCTCAGAAA-----TGGCTGGCTTCTGAC	524
QY	361	AGGTCTCCCGCCCAAGGGGCGGGGCTGTGAGAGGGGGGGGGGAGATTCTCTCCCGCGTG	420
Db	523	AGG-----CTCCGACACAGTGGCGGGGCTTGAGATGGTGGAGGG-----ATTTCCTCCCATG	472
QY	421	CAAGGTATTTTCCCTCATATATC-CGGTTTCTCCCTCTCCCAATTTTTCACGAGGGGGCGCGC	479
Db	471	CAAAAGTATTTATCATCATCATCATCTGACTACCTCATCTCCCAACCTCTTCCATTTGGCGTCCG	412
QY	480	CGTGGCTGGGT 491	
Db	411	CCTGTGTGGGT 400	
RESULT 3			
ID	AAAI6224		
AC	AAAI6224	standard; DNA; 610 BP.	
XX	AAAI6224:		
DT	14-JUN-2000	(first entry)	
XX			
DE		Human colon cancer differentially expressed nucleotide sequence #229.	
KW		Colon cancer; detect; differential expression; human; treatment;	
KM		detect mutation; non-invasive diagnostic method; ds.	
XX			
OS		Homo sapiens.	
XX			
PD	MO200012702-A2.		
XX			
PD	09-MAR-2000.		
XX			
PF	30-AUG-1999;	99WO-US19424.	
XX			
PR	31-AUG-1998;	98US-0098639.	
PR	27-JAN-1999;	99US-0117393.	
XX			
FA	(FARB)	BAYER CORP.	
XX			
PI	Endege WO,	Steinmann KE, Astle JH, Burgess CC, Carroll E;	
PI	Carino TJ,	Dwivedi P, Ford DM, Lewis ME, Molino GA, Monahan JE;	
PI	Schlegel R;		
XX			
DR	WPI: 2000-256641/22.		
XX			
PT		Novel nucleic acids and proteins for identifying therapeutic agents	
PT		useful for treating and diagnosing cancer, especially colon cancer	
XX			
PS	Claim 16;	Page 215; 345pp; English.	
XX			
CC		This sequence represents a human nucleotide sequence which is	
CC		differentially expressed in colon cancer cells compared to the expression	
CC		levels in normal cells. The nucleotide sequence can be used as a source	
CC		of primers and probes. The nucleotide sequence is useful for determining	
CC		the phenotype of a cell by detecting the differential expression of the	
CC		sequence relative to a normal cell. The probes derived from the sequence	
CC		can also be used to determine the phenotype of cells in a sample. Probes	
CC		and antibodies which hybridise to the nucleotide sequence can also be	
CC		used to determine the phenotype of a cell. The primers are useful for	
CC		detecting a mutation in a test nucleotide sequence and also for detecting	
CC		cancer, preferably colon cancer. Antibodies against the protein encoded	
CC		by the nucleotide sequence can also be used in a method to detect colon	

CC	cancer.	The diagnostic method is non-invasive and accurate for diagnosing
CC	colon cancer at an early stage.	
XX	Sequence 610 BP; 161 A; 140 C; 139 G; 159 T; 11 other;	
XX	Query Match 11.3%; Score 72.4; DB 21; Length 610;	
XX	Best Local Similarity 58.0%; Pred. No. 6.3e-08;	
XX	Matches 296; Conservative 0; Mismatches 173; Indels 41; Gaps 8	
QY	5 TTTTTTTTTTTTTTTTTTTTTTTCCAAACAAAATTTTTTGGCCCTTAAACCCCTTG 64	
DB	6 TTTTTTTTTTTTTTTTTTTTTTTGGACAGCTAAATAATTTTATGCTCTTTAAAGCCTTA 65	
OY	65 GCGCCCTTTAAATAATGGAAGACACTGAAAGTGCACGCGGGGAGGAAAAAACCAAAAA 124	
DB	66 GCGCCCTATGACAAAATGAAAGAGACTGAAATGTACAGCGGGGAGGAAAGAAACAGAAAGA 125	
OY	125 ACAGATTAATAAATGTAGAGGGGGCGGAGGGGAGGAAATACCAATATTTCTCTCCGAG 184	
DB	126 TAAGA-----ATGAGGTGTGTCAAGTTGGGGGAAATTAAGGAAATATTTCTCTCC--- 173	
OY	185 GGAGAGAGTCCCGCCACAGCGCGCCCATCCCGAGTGAAGTGTGTGCGACCCCAACACAGGG 244	
DB	174 --AGGGTGAAGTCTCTCAGACTGGTGTCTCATGCCCATGATGAGTTGCCAACACCAACACAGGCT 231	
OY	245 GCGGCGTGAAGTCCCCCGCGGTGACATAGTGTGTGAAATCTTGCCAGACTTGGGTGATCC 304	
DB	232 GGTGACTTCCCGTCCGCACTAGTCAAGTGAATTCGACAGAT-----AGGGTAACC 281	
OY	305 TCCCTTTATCGTTTATTTCTTTCCCCCTCAAAATGGGCTGGTGTCTCTTCCCGAAGT 364	
DB	282 TCACATTTACAGTTAATAATCTTTCACACTGAGAA-----TGCTGTGCTTCTGACAGG- 334	
OY	365 GTCCCGCCCAAGGGGCGGGGCTGAGAGAGGGGGGGGAAATCTCTCCCGCGTGCAAG 424	
DB	335 ---CTCGCACAATGGCGGGGCTGTGAAATGGTGGAGG---ATTCTCTCCCATGCAAA 387	
OY	425 GATTTTCTCATATTC-CGGTTTCTCTCTTCCCAATTTTTCGCCAGGGGGGCGCGCGCTG 483	
DB	388 GAAATTCATCATCATCATCTGNTACTCTCACATCCCAACCTCTCCATGTTGGGCTCGGTCGCC 447	
OY	484 GGTGGGTT--TGGCCCGCACCCCAACTTTTG 511	
DB	448 TGTGGGGTCTATGACCCCAATCCAACTGATG 477	
XX	RESULT 4	
XX	ABK44094/C	
XX	ID ABK44094 standard; cDNA; 534 BP.	?
XX	XX ABK44094;	
XX	DT 21-MAY-2002 (first entry)	
DE	CDNA #34 encoding human pancreatic tumour protein.	
KW	Human; pancreatic tumour protein; immune response; pancreatic cancer;	
XX	development of cancer; cancer progression; cytostatic; gene; ss.	
OS	Homo sapiens.	
XX	WO200212331-A2.	
XX	PD 14-FEB-2002.	
XX	PF 06-AUG-2001; 2001WO-US24619.	
XX	PR 07-AUG-2000; 2000US-223130P.	
XX	PR 30-JAN-2001; 2001US-265447P.	
XX	PA 15-MAY-2001; 2001US-291201P.	
XX	(CORI-) CORIXA CORP.	

Query Match Similarity 8.7% Score 55.4; DB 24; Length 546;
Best Local Similarity 60.1%; Pred. No. 0.00073;
Matches 107; Conservative 0; Mismatches 64; Indels 7; Gaps 2;

OY 11 TTTTNTTTTTTTTTTTTTTCACAAACAATAATTTTTTGCCCTTAACACCCTTGGCGGT 70
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 337 TTTTNTTTTTTTTTTTTTTTTTCGACTAATAATTTTTATGNTTTTAAANNCCTTAGGCCGN 396

OY 71 TTTAAAAATGCAAAAGCAGTGAAGTGCACGCGGGGAGAAAAAACCAAAAACAGAT 130
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 397 TTGANAANAANGAANAACCTGAATG---ACACGGGGGNGGANGAACCNGAANNANGAT 453

OY 131 AAAAATGTGAGGGGCGGAGGTGGGGGAATPACACCAAATTTCTCTCCGAGGGAG 188
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 454 NNNA-----TNGGGGGGCGNCAAGTGGGGGAATTAACNNANATTTTNTTTCANGGGG 507

RESULT 8
ABV61015
ID ABV61015 standard; CDNA: 294 BP.

XX AC ABV61015;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 61006.
XX KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW Pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PE 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-235281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI: 2001-662795/76.
XX XX
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX PS
XX PM Claim 1; Page 11596; 11750pp; English.
XX XX

The invention relates to an isolated nucleic acid molecule (I) comprising
a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
patient;
(I) is also useful as a pharmacodynamic or pharmacogenomic marker.

SQ	Sequence 294 BP; 55 A; 53 C; 78 G; 105 T; 3 other;
	Query Match 8.6%; Score 54.6; DB 23; Length 294; Best Local Similarity 54.8%; Pred. No. 0.00096; Matches 108; Conservative 0; Mismatches 89; Indels 0; Gaps 0
QY	1 TTTTTCCTTTTTTTTTTTTTTTTTTTTCCAAACAAAATTTTGGCCTTAAGACC 60 DB 72 TTTTTCCTTTTTTTTTTTTTTTTTTTGCGGAAAAAATTTTCTTCCCCC 131
OY	61 CTGGGCGCTTTAAAAAATGAAGAAGCACTGAAGAAGCACGCGGGGAGAAAAAACCA 120 DB 132 GGGGGGGGGGAAAAAAGAAAAAACCCTTGCGGGGGGGGGGGGCTTTTAACCC 191
OY	121 AAAAACAAGATAAAAAAGTAGAGGGGCCGAGAGGTGGGGGGAATTACACAAATTTCTCTCC 180 DB 192 CCCCTTTTGGGGGGGGGGCCCCAAAAAAGGGGGGGGAAAAAAGATTTTGGG 251
OY	181 CGAGGGAGAGACTCCCCC 197 DB 252 GGGGGGGGAGGCCCCC 268
RESULT 9	
AAS07790	AAS07790 standard; DNA; 256 BP.
XX AC	AAS07790;
XX XX	23-OCT-2001 (first entry)
DE	Cervical cancer pre-malignant condition DNA marker #89.
XX KW	Cervical cancer; pre-malignant condition marker; tumorigenesis: CIN; ds-
KW	cervical intraepithelial neoplasia; squamous intraepithelial lesions;
KW	polymerase chain reaction; PCR; enzyme linked immunosorbent assay; ELISA;
OS	anticancer therapy; carcinogen; antisense inhibition.
PN	Homo sapiens.
XX	WO200142792-A2.
PD	14-JUN-2001.
XX	08-DEC-2000; 200OWO-US33311.
PR	08-DEC-1999; 99US-0169811.
PR	21-DEC-1999; 99US-0171330.
PR	14-MAR-2000; 200OUS-0189113.
PR	31-MAR-2000; 200OUS-0193943.
PR	12-MAY-2000; 200OUS-0203772.
PR	09-JUN-2000; 200OUS-0210820.
PR	21-JUL-2000; 200OUS-0220113.
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI	Schlegel R, Deeds J, Berger A, Zhao X;
DR	WPI: 2001-367889/38.
P7	Cervical cancer protein markers useful for the diagnosis, prevention
XX	and treatment of cervical cancers, especially cervical intraepithelial
XX	neoplasia or squamous intraepithelial lesions -
PS	20; Page 413; 436pp; English.
XX	The sequence represents a cervical cancer pre-malignant condition marker.
CC	These markers encode proteins that are over expressed during
CC	tumourigenesis. The proteins and their corresponding nucleic acid
CC	sequences can therefore be used for the diagnosis, prevention and
CC	treatment of cervical cancers, particularly cervical intraepithelial
CC	neoplasia (CIN) and squamous intraepithelial lesions (SIL). The sequences
CC	may be used as markers in diagnostic assays to detect cancerous

Db 232 GCTGACTTCCCTGCTGACATGATGAACTTGACAGCAT-----AGGGTAACC 281
OY 305 TCCCTTATGTTTATTTCTTCCCTCCCAAAATGGGCTGCTGCTTCCGAGCT 364
Db 282 TCAATATGATTAATATCTTCCACTCAGAAA-----TGCTGCTCTTCCACAGC- 334
OY 365 GTCCCTCCCAAGGGGCGGCTGAGAGGGGGGGGATTTCTCCCTCCGTCGACG 424
Db 335 ---CTGACAGAGTGGCGGCTTGANATGTGTAGAGG---ATTCTCTCCCATGCAA 387
OY 425 GTATTCTCATATC-CGGTTTCTCTCTCCCAATTTTCCAGAGGGGCGCGCCGTG 483
Db 388 GTATTCTCATATCAGTACTGATCTCCCACTTCTCCATTTGGGCTCGGTGCCCTG 447
OY 484 GTGGGTT--TGCGCCCAACCACTTTG 511
Db 448 TGTGGGTGATGAGCCCAATCAGATG 477

RESULT 2

US-09-385-982-224
; Sequence 224, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(622)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-224

Query Match 9.7%; Score 62; DB 4; Length 622;
Best Local Similarity 60.3%; Pred. No. 6.1e-08;

Matches 111; Conservative 0; Mismatches 64; Indels 9; Gaps 1;

OY 2 TTTTTTTTTTTTTTTTTTTTTTCCAAACAAATTTTTGGCCCTTAACCC 61
Db 19 TTTCTTTTTTTTTTTTTTTTTTTTTTGCNNCTAAATNNGATTCCTTAAAGCC 78
OY 62 TTGGCGCGTTTAAATAAGCACTCAAAAGTCAGCGCGGGAGGAAAAACCAA 121
Db 79 TTAGCGCGNATGCAAAATGANNAGCTGAATGACACGCGGAGAGAAACAGANMA 138
OY 122 AAAACGATAAATAAGTGAAGGGCGGAGGTGGGGGATACACCAATATTCTCTCC 181
Db 139 AGATAGA-----ATGAGGTGTGTCAGTGTGGGGAATTAAGCAATATTCNCTCC 189
OY 182 GAGG 185
Db 190 NNGG 193

RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463

; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOMBOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 8.9%; Score 56.6; DB 1; Length 7218;
Best Local Similarity 3.8%; Pred. No. 5.7e-06;

Matches 14; Conservative 212; Mismatches 141; Indels 0; Gaps 0;

OY 271 AGTTCGTGAATCTTCCAGACTTGGGTGATCCCTTATCGTTATTTCTTCCG 330
Db 1047 AGGTGAGGAGGAGCTTGCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1106
OY 331 CCTCAAAATGGCGTGTCTCTCTCGAAGGTGCCCCCAAGGGCGCGGGCTGGA 390
Db 1107 TT 1166
OY 391 GAGGGGGGGGGGATTCCTCCCGCGCAAGATTTCTCATATTCGCTTCTCT 450
Db 1167 TT 1226
OY 451 CTCCTCAATTTTCCAGAGGGGCGCGCGGTGGGTGGCGCCCAACCACTTTT 510
Db 1227 TT 1286
OY 511 GTTCGTACAGGTTTCCGCGGGGGCGGAGGTTCTTCCCTGCTCTCCCTCC 570
Db 1287 TT 1346
OY 571 TTTCAAGGCGCTTTGGGCCCAATGCTTCCGCGTTGTGTCACAGGAGGCTG 630
Db 1347 TT 1406

QY	631	TCTCGCT	637
		:::::	::
Db	1407	YYYYYY	1413

RESULT 4
US-08-984-919A-10/c
; Sequence 10, Application US/08984919A
; Patent No. 638374

GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
TITLE OF INVENTION: PARASITIC NEATODE TRANSLUPTAMINASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

```

1. COMPUTER READABLE FORM:
2. MEDIUM TYPE: Floppy disk
3. COMPUTER: IBM PC compatible
4. OPERATING SYSTEM: Windows 95
5. SOFTWARE: Wordperfect for Windows, Version 7.0
6. CURRENT APPLICATION DATA:
7. APPLICATION NUMBER: US/08/984, 919A
8. FILING DATE: 04-DEC-1997

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: INFORMATION FOR SEQ. ID NO.: 10
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: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1466 nucleotides
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: cDNA
:   FEATURE:

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Query Match	8.5%	Score	54	DB	4	Length	1466
Best Local Similarity	62.7%	Pred.	No.	1.4e-05			
Matches	84	Conservative	0	Mismatches	50	Indels	0
						Gaps	0

RESULT 5
US-08-984-919A-12
; Sequence 12, Application US/08984919A

Patent No. 6383774
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,919A
FILING DATE: 04-DEC-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1466 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-984-919A-12

Query Match	8.58;	Score 54;	DB 4;	Length 1466;
Best Local Similarity	62.78;	Pred. No. 1.4e-05;		
Matches 84;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;

RESULT 6
 US-08-781-420-10/c
 : Sequence 10, Application US/08781420
 : Patent No. 6248672
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Mehra, Kapil
 :
 : TITLE OF INVENTION: Parasitic Nematode Tryptophanase
 : TITLE OF INVENTION: Proteins, Nucleic Acid Molecules and
 : NUMBER OF SEQUENCES: 21
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Carol Talkington Verser, Ph.D.
 :
 : ADDRESSEE: Heska Corporation
 : STREET: 1825 Sharp Point Drive

```

RESULT 7
US-08-781-420-12
: Sequence 12, Application US/08781420
: Patent No. 6248872
: GENERAL INFORMATION:
: APPLICANT: Chandrashekar, Ramaswamy
: APPLICANT: Mehra, Kapil
: TITLE OF INVENTION: Parasitic Nematode Triclutamine
: TITLE OF INVENTION: Proteins, Nucleic Acid Molecules and
: TITLE OF INVENTION: Uses Thereof
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carol Talkington Verser, Ph.D.
: ADDRESSEE: Heska Corporation
: STREET: 1825 Sharp Point Drive
: CITY: Fort Collins
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80525
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: WordPerfect for Windows, Version 7.0

```

RESULT 8
 US-08-874-102-10/C
 Sequence 10, Application US/08874102
 Patent No. 6303644
 GENERAL INFORMATION:
 APPLICANT: Ramaswamy Chandrashekar
 APPLICANT: Kapil Mehta
 TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
 TITLE OF INVENTION: PROTEINIC, NICOTIC ACID MOLECULES,
 TITLE OF INVENTION: AND USES THEREOF
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Wordperfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/874,102
 FILING DATE: 12-JUN-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: HW-2-C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 10:

Query Match	8.3%	Score 53.2	DB 10	Length 798
Best Local Similarity	58.5%	Pred. No. 0.0025		
Matches 273	Conservative 0	Mismatches 158	Indels 37	Gaps 9
OY	23	TTTTTCCCAACAAAAATTTTTTGGCCCTTAATACCCTTGCGCCCTTTAAAAAATGA	82	
Db	798	TTTTTTCGACACTAAAAATTTTTATTGCTTTAAAGCCTTAAGCCGATGACCAAAATGA	739	
OY	83	AAAGCAGTGAAGTGCACCGCGGGAGGAAAAACCAAAAAACGATTAAGAACTGGAGG	142	
Db	738	AGAGACTGAATAGACTACCGGGAGGAGAAACAAAGAAAGATTAAGATGAGTGATCA	679	
OY	143	GGGCGGAGGTTGGGGGAGATACACCAAAATATTCTCCGAGGAGAGATGCCCCACAGC	202	
Db	678	-----GGTTGGGGGGAATTAGCGAATATTCTTTCC--AGSGTAGTGCGACACTG	629	
OY	203	GGCGCCCATCCCCAGTACTGTGTGGGACACCCCAACACGSGGCGGCTGACTCCCCCG	262	
Db	628	GTCTATGATCCCATGTATGAGTT-----GGACACCAACACAGGCTCTACTTCCCTCG	574	
OY	263	CGTGACATAGTTCCGGAATCTTGGCAGACTGGGGTGAACCTCCCTTTATCGTTTAT	322	
Db	573	CACATAGTAGTG-----AACTTTCAGACATAGG--GTAACTCTCAATTACAGTATAT	521	
OY	323	TCCTTCCCCCTCAAAATGGGCTGTCTTCTCCGAAGGTGTCCCCCAAGGGGCGG	382	
Db	520	CTTTCACACTTCAGAAA-----TGCTGTGCTTCTTCGACAGG---CTCGACAGTGGCG	471	
OY	383	GGGCGTGAAGGGGGGGGGGATTCCTCCCCCGGTGAAGATTTTCATCATAT--CG	441	
Db	470	GGGCTTGAGATGTGTGAAGGATTTCT-----CTCCATGCAAAAGTATATTCACATCACT	415	
OY	442	GTTCCTCTCCCAATTTTTTCCAGGGGGGCGGCGCTTGAGGTT	491	

AUTHORS	Hedde,P., Qi,R., Abernathy,K., Dharap,S., Gasparid,R., Gay,C., Holt, J.E., Saeed,A.I., Shatrov,V., Lee,M.H., Yastman,T.J. and Quackenbush,J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20150, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 25
FEATURES	Seq primer: Reverse. Location/Qualifiers 1..490 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE_resequences_MAGA" /note="Vector: pBluescriptSkm"
BASE COUNT	138 a 118 c 103 g 131 t
ORIGIN	
Query Match	10.5% Score 67.2; DB 10; Length 490; Best Local Similarity 64.7%; Pred. No.0.5;
Matches 119; Conservative 0; Mismatches 58; Indels 7; Gaps 1;	
OY 2	TTTTTTTCTTTTTTTTTTTTTTTTCACAAATAATTTTGCCCTTAATAACC 61 Db 375 TTTTATTATTATTAAAAATTTTGTGCAAGACTAAAATTTATGCTCTTAACCG 316
OY 62	TTGGCCGCTTTAAAAAATGCAAAAGCAGTGAAGTGCAACGCCGGAGAGAAAAACA 121 Db 315 TTAGCCCTATGCACAAAATGAAGACCTGAATGACACCGGGAGGAGAA-----AAC 263
OY 122	AAAAAGATTAATAAGTAGAGGGGCCGAGGGGGGGGGGGAATACACCAATATTCCTCCC 181 Db 262 AGAAGAAAGATACAGATGAGGTCTGTCTACTGTGGGGGAATTAMCGGAATATCTCTTCC 203
OY 182	GAGG 185
DB 202	AGGG 199
RESULT 4	
BOS26160	394 bp mRNA linear EST 10-JUN-2002
LOCUS	NISC.noi4g06.x1.NICH_XGC.Emb8.Silurana.tropicalis.cDNA clone
DEFINITION	IMAGE:5361171.3, mRNA sequence.
ACCESSION	BOS26160
VERSION	BOS26160.1 GI:21385029
KEYWORDS	EST.
SOURCE	western clawed frog.
ORGANISM	Silurana tropicalis Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Silurana. 1 (bases 1 to 394) NIH-XGC http://image.llnl.gov/image/html/xenopuslib.info.shtml. National Institute of Child Health and Human Development, National Cancer Institute, Xenopus Gene Collection unpublished (2002) Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov cDNA Library Preparation: CDNA library Arrayed by: The I.M.A.G.E. Consortium/LNL Sequencing center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. consortium/LNL at: info@image.llnl.gov Plate: LHAM1970 row: M column: 12 Seq primer: -21M13 forward primer (ABI).
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES		location/Qualifiers
SOURCE		1..394
		/organism="Silurana tropicalis"
		/db_xref="taxon:8364"
		/clone="IMAGE:5381171"
		/clone_lib="NICHD_XGC_Emb8"
		/tissue_type="taadpole"
		/dev_stage="embryo, stages 40-45"
		/lab_host="DH10B (phage-resistant)"
		/note="Vector: pCMV-SPORT6.ccdp; Site_1: NotI; Site_2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
BASE COUNT	143 a	49 c 63 g 139 t
ORIGIN		
Query Match	10.4%; Score 66.4;	DB 14; Length 394;
Best Local Similarity	60.6%; Pred. No. 0.79;	Mismatches 71; Indels 0; Gaps 0;
Matches 109;	Conservative 0;	
QY 1	TTTTTTTTTTTTTTTTTTTTTTCCAAACAATAATTTTGCCCTTAACAC 60	
Db 56	TTTCCC 115	
QY 61	CTGGGCGCGTTAAAAAATGCAAAAGCCTGAAGTCACGCCGGGAGAAAACCAA 120	
Db 116	CCCCGGGGGTATTAAAAAAGAAAAAAGAAAAAAGGGGGGGAAGAAAAA 175	
QY 121	AAAAACAGATTAAAAAGTGAGGGGCGGAGGGGTGGGGGAATACACAAATATTCCTGC 180	
Db 176	AAAAAAAAAAAAAAAAAGGGGGGGGGGCGCTTTTTTTTTTCCAAAAAAGAAAAAACCCACC 235	
RESULT 5		
A1445576		
LOCUS		
DEFINITION	A1445576	521 bp mRNA linear EST 13-APR-1999
	tj26a01.x1 NCI-CGAP-Gas4 Homo sapiens cDNA clone IMAGE:2142600 3'	
	similar to gb:L15533_rnal PANCRAETITIS ASSOCIATED PROTEIN 1	
	PRECURSOR (HUMAN);, mRNA sequence.	
ACCESSION	A1445576	
VERSION	A1445576.1	GI:4289178
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 521)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU at: www-bio.llnl.gov/dbcp/image/image.html Insert Length: 930 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 383.	
FEATURES		
SOURCE		
	Location/Qualifiers	
	1..521	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:2142600"	
	/clone_lib="NCI CGAP Gas4"	
	/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"	
	/lab_host="DH10B"	

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

1. .412

Query Match	9.68;	Score 61.4;	DB 10;	Length 412;
Best Local Similarity	68.28;	Pred. NO. 4.1;		
Matches 118; Conservative	0;	Mismatches 46;	Indels 9;	Gaps 2;

133 AAGTGGAGGGGCGGAGGGTGGGGGGAATACACCAATATTTCTCCGAGG 185
Oy 118 A-----TGAGTGGTACAGTTGGGGCAATTAGCGAATATTTCTTCCAGG 164
Db

RESULT 10	AL513913	AL513913	456 bp	EST_13-FEB-2001
LOCUS	AL513913	LTI_NFL006_PL2	Homo sapiens cDNA clone CLOBAD006ZF12 3 prime, mRNA sequence.	
DEFINITION	AL513913	LTI_NFL006_PL2	Homo sapiens cDNA clone CLOBAD006ZF12 3 prime, mRNA sequence.	

ACCESSION	AL513913
VERSION	AL513913.1
KEYWORDS	GI:12777407
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Euarctota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1. (bases 1 to 456)	Li, W. B., Gruber, C., Jesse, J., and Polay, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

1. .456

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C10BA0066F12"
/clone_id="L71_NF1006.PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Division of Invitrogen 9800 Medical Center Drive

Query Match	9.6%	Score 61.4	DB 9	length 456
Best Local Similarity	47.4%	Pred. No. 3.8		
Matches 102	Conservative 23	Mismatches 90	Indels 0	Gaps 0

[illegible]

RESULT 11	LOCUS	DEFINITION
A1919058	495 bp	mRNA
A1919058	495 bp	linear
tut77c08.x1	NCI_CGAP_Gas4	mouse sapiens cDNA clone IMAGE:2257070 3'
	similar to SW:PRRB_HUMAN P02814	PROLINE-RICH PEPTIDE P-B.; contains element MSRI repetitive element; mRNA sequence.

ACCESSION	AI919058
VERSION	AI919058.1
	GI:5638913

KEYWORDS	EST.
SOURCE	
ORGANISM	
human.	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	
1 (bases 1 to 495)	

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: c940ps-remail.llnl.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at: www.dio.llnl.gov/bbrp/image/image.html
Insert length: 2965 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 289.

1. .495

BASE COUNT	121	a	104	c	113	g	157	t
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2257070" /clone_1b="NCL CGAP_Gas4" /tissue_type="poorly differentiated adenocarcinoma with signed ring cell features" /lab_host="DH10B" /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"							

Query Match	9.6%: Score 61.4; DB 9; Length 495;
Best Local Similarity	51.7%: Pred. No. 3.5; Mismatches 131; Indels 0; Gaps 0;
Matches 140; Conservative	0; Mismatches 131; Indels 0; Gaps 0;
QY 1	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCAAACAAAATTTTTTGCGCCCTTAAAC 60
Db 75	TTTCC 134
QY 61	CTTGGCCGCTTAAAAATGCAAAAGCACTGAAATGCAACGCGGGGAGGAAAAACCA 120
Db 135	CCCCGGCTTTTAAAAAAGGAAACCCCCCGGGGGGGGGGAGGAAAAACCCCCAA 194
QY 121	AAAAACAGATAAAAAGTGGAGGGGCCGAGGTGGGGGGAATACACAAATTCCTCC 180
Db 195	AAAAAACCCAAAAAATTTTGGGAAAAAAACCGGGGAAAAACCCCCCTATATATTG 254
QY 181	CGAGGAGAGTCCCGCCACAGCGCCCGCCATCCCACTGAGTGTGTGGACCCCAACA 240
Db 255	TGCAAAAAAAGAAACCCCTGGGGGGGGGGGGGGGAAAAAAGGAAAAAAG 314
QY 241	CGGGCGGGCGTGACTCCCCCGCGCGAGATATA 271
Db 315	GGGGGCCCCCCCCCCCCCGGGGAAAAAA 345
RESULT 12	
LOCUS	BF036274 919 bp mRNA linear EST 20-OCT-2000
DEFINITION	601459416F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863258 5', mRNA sequence.
ACCESSION	BF036274
VERSION	BF036274.1 GI:10744182
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 919)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cgapds-remail.nih.gov
	Tissue Procurement: DCTD/DTF
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
	http://image.lnl.gov
	Plate: LHAM9602 row: o column: 03
	High quality sequence stop: 148.
FEATURES	Location/Qualifiers
SOURCE	1..919
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:3863258"
	/issue_lib="NIH_MGC_66"
	/issue_type="adenocarcinoma"
	/lab_host="DH10B (phage-resistant)"
	/note="Organ: ovary; Vector: pCMV.SPORT6; site_1: NciI; site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 Kb. Library constructed by Life Technologies."
BASE COUNT	328 a 216 c 231 g 144 t
ORIGIN	
Query Match	9.6%: Score 61.4; DB 12; Length 919;
Best Local Similarity	52.1%: Pred. No. 2; Mismatches 126; Indels 0; Gaps 0;
Matches 137; Conservative	0; Mismatches 126; Indels 0; Gaps 0;
QY 1	TTTTTTTTTTTTTTTTTTTTTTTTTCCAAACAAAATTTTTTGCGCCCTTAAAC 60

[illegible]

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using SW model

(without alignments)
4490.451 Million cell updates/sec

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Perfect score: 2/0
Sequence: 1 acaaagctttttttttttt.....taaacagacagtcantctn 270

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Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Pre-processing:	Minimum Match	0%	10%	20%	30%	40%	50%	60%	70%	80%	90%	100%
Post-processing:	Minimum Match	0%	10%	20%	30%	40%	50%	60%	70%	80%	90%	100%

Listing first 45 summaries

Database : GenEmbl.*

GenEmbl: *

- 1: gb_ba: *
- 2: gb_hhg: *
- 3: gb_ln: *
- 4: gb_om: *
- 5: gb_ov: *
- 6: gb_pat: *
- 7: gb_ph: *
- 8: gb_pl: *
- 9: gb_pr: *
- 10: gb_ro: *
- 11: gb_sts: *
- 12: gb_sy: *
- 13: gb_un: *
- 14: gb_vl: *
- 15: em_ba: *
- 16: em_fun: *
- 17: em_hum: *
- 18: em_in: *
- 19: em_mu: *
- 20: em_om: *
- 21: em_or: *
- 22: em_ov: *
- 23: em_pat: *
- 24: em_ph: *
- 25: em_pl: *
- 26: em_ro: *
- 27: em_sts: *
- 28: em_un: *
- 29: em_vl: *
- 30: em_hhg_hum: *
- 31: em_hhg_ln: *
- 32: em_hhg_other: *
- 33: em_hhg_mus: *
- 34: em_hhg_pln: *
- 35: em_hhg_rod: *
- 36: em_hhg_mam: *
- 37: em_hhg_vrt: *
- 38: em_sy: *
- 39: em_hhg_hum: *
- 40: em_hhg_mus: *
- 41: em_hhg_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result

No.	Score	Match Length	DB	ID	Description
1	268	99.3	2761	6	AX338100
2	81.6	30.2	2751	6	AX100254
3	81.2	68205	30.1	6	AX116830
4	80	29.6	160413	2	AX114254
5	79.4	625	635	6	BC032803
6	77.6	2132	2	AB072776	
7	77	28.7	179601	2	AC117277
8	76.8	28.4	99006	2	AC096254
9	76.6	1661	6	AX025906	
10	76	28.1	440	6	AX184953
11	76	28.1	1464	6	IR2005397
12	76	28.1	1621	9	HSB003093
13	76	28.1	1705	9	BC032249
14	76	28.1	186866	2	AC106085
15	75.8	28.1	1069	9	BC009520
16	75.8	28.1	1872	6	AR205050
17	75.4	27.9	186277	2	AC111651
18	75.2	27.9	139736	2	AC112779
19	74.6	27.6	1146	9	HSB02966
20	74.6	27.6	1541	6	E04233
21	74.5	27.6	60087	2	AC117320
22	74.4	27.6	1842	9	AK026885
23	74.4	27.6	2152	10	BC005532
24	74.2	27.5	398	17	AF116644
25	74.2	27.5	764	9	BC030244
26	74.2	27.5	2037	9	BC001963
27	74.2	27.5	2571	17	AF113676
28	74.2	27.5	3331	9	HSB08395
29	74	27.4	1673	10	BC010324
30	74	27.4	2126	9	BC016330
31	73.8	27.3	485	6	AX092312
32	73.8	27.3	485	6	AX376118
33	73.8	27.3	485	6	AX403358
34	73.8	27.3	1734	6	AX092320
35	73.8	27.3	1734	6	AX358902
36	73.8	27.3	1734	6	AX362395
37	73.8	27.3	1734	6	AX376134
38	73.8	27.3	1734	6	AX403750
39	73.8	27.3	1734	6	AX454564
40	73.8	27.3	1734	6	AX491042
41	73.8	27.3	129632	2	AC133165
42	73.6	27.3	1072	9	BC001418
43	73.6	27.3	1072	9	BC013953
44	73.6	27.3	1969	9	BC007355
45	73.2	27.1	1284	9	BC011910
					AX338100 Sequence
					AX100254 Sequence
					AX116830 Mus musculus
					AX114254 Rattus norvegicus
					BC032803 Homo sapiens
					AB072776 Macaca fascicularis
					AC117277 Rattus norvegicus
					AC096254 Rattus norvegicus
					AK025906 Homo sapiens
					AX184953 Sequence
					AL389978 Homo sapiens
					AL713720 Homo sapiens
					BC032249 Homo sapiens
					AC106085 Rattus norvegicus
					BC009520 Homo sapiens
					AR205050 Sequence
					AC111651 Rattus norvegicus
					AC112779 Rattus norvegicus
					AL137744 Homo sapiens
					E04233 DNA encoding
					AC117320 Rattus norvegicus
					AK026885 Homo sapiens
					BC005532 Mus musculus
					AF116644 Homo sapiens
					BC030244 Homo sapiens
					BC001963 Homo sapiens
					AF113676 Homo sapiens
					AL832088 Homo sapiens
					BC010324 Mus musculus
					BC016330 Homo sapiens
					AX092312 Sequence
					AX376118 Sequence
					AX403358 Sequence
					AX092320 Sequence
					AX358902 Sequence
					AX362395 Sequence
					AX376134 Sequence
					AX403750 Sequence
					AX454564 Sequence
					AX491042 Sequence

RESULT 1
AX338100

LOCUS	AX338100	270 bp	DNA	linear	PAT 09-JAN-2002
DEFINITION	Sequence 13 from Patent WO0175169.				
ACCESSION	AX338100				
VERSION	AX338100.1	GI:18128731			

ORGANISM

AUTHORS

imaging and treating stomach cancer

[illegible]

```

Db      2340    AAGCGGGGGAATGTGGCAAGACGAGCAGGAGGCAGACCCCC   2301
|       |         |||||          |||        |||     |   |||| 
RESULT_3                                     ACI16830           68205 bp   DNA             linear   HTG-02-Apr-2002
ACI16830                                locus                               Mus musculus clone RP24-375115, LOW-PASS SEQUENCE SAMPLING.
DEFINITION                                ACI16830
VERSION                                  ACI16830..1 GI:19842084
KEYWORDS                                 HTG; HTGS_PHASED.
SOURCE                                   Mus musculus.
ORGANISM                                Mus musculus.
Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarchontia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS                                  Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE                                    1 (bases 1 to 68205)
JOURNAL                                  Mus musculus clone RP24-375115
PUBLISHED                              Unpublished
COMMENT                                  2 (bases 1 to 68205)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Batra,N., Bastien,V., Bloom,T., Boguslavsky,I., Bookhalter,B., Brown,A., Camarero,J., Campiano,A., Chang,J., Charazni,P., Choquel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A., Cooke,P., Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., Fitzgugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Gold,S., Goyletze,M., Graham,L., Grand-Pierre,N., Hagos,B., Harton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Knat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., MacDonald,P., Major,J., Marguis,N., Matthews,C., McCarthy,M., McKean,P., McKernan,K., Meldrum,J., Menius,L., Milnova,T., Miengua,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,O'Neil,D., Oliver,J.C., Peterson,K., Punthanang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rossetti,M., Roy,A., Santos.R., Schauer,S., Schnuppach,R., Seaman,S., Severly.P., Spencer.B., Strange-Thomann.N., Stojanovic.N., Strauss.N., Subramanian.A., Talamas.J., Tesfaye.S., Theodore.U., Topham.K., Travers.M., Travis.N., Trigilio.J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman.D., Ye.W.J., Young.G., Zainoun.J., Zemбек.L., Zimmer,A. and zody.M.
Direct Submission
Submitted (02-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 0214L, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: I25584
Center clone name: J75_L15
-----
NOTE: This record contains 85 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
-----
1 695: contig of 695 bp in length
* 696 795: gap of 100 bp
* 796 1505: contig of 710 bp in length
* 1506 1605: gap of 100 bp
* 1606 2306: contig of 701 bp in length

```


Qy 127 AGCGCCGCGAGCGGCTGACAGCGGCGACCCCGAGACCGCGCGCAC 182
 Db 28649 GCGGCGCGCGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCTGGTGGCGTCCGCC 28704

RESULT 4

AC114254

LOCUS

DEFINITION

AC114254 160413 bp DNA linear HTG 13-JUL-2002
 Rattus norvegicus clone CH230-345K18, *** SEQUENCING IN PROGRESS
 *** 44 unordered pieces.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC114254.2 GI:21738359
 HTG: HTGS_PHASE1.
 Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE

AUTHORS

1 (bases 1 to 160413)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbara,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Boyle,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkett,C., Butrell,K.L., Byrd,N.C.,
 Cartron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Eathart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,D., Foster,P., Frantz,P.,
 Gabriel,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hughes,M., Holloway,C., Hollins,B.,
 Homsl,F., Howard,S., Huber,J., Huylk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Kovach,J., Kovar,C.,
 Kirovich,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisedge,H.,
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mawhinley,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokwkw,S., Oguh,M., Okwuonu,G.,
 Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Qules,M., Ren,Y.,
 Rivers,M., Rojas,A., Rojubenkan,I., Rolfe,M., Ruiz,S., Savery,G.,
 Scherer,S., Scott,G., Shen,H., Shooshitari,N., Sisson,I.,
 Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Swalek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gdbbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission
 Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 160413)
 Worley,K.C.
 Direct Submission
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 12, 2002 this sequence version replaced gi:19224581.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project information
 Center project name: GOXR
 Center clone name: CH230-345K18
 ----- Summary Statistics

Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 106846 bases at least Q40
 Consensus quality: 111742 bases at least Q30
 Consensus quality: 116349 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 44 contigs. The true order of the pieces
 * is not known and their order in this sequence report is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1448	contig of 1448 bp in length
1449	1548	gap of unknown length
1549	2807	contig of 1259 bp in length
2807	2908	gap of unknown length
2908	3989	contig of 1082 bp in length
3989	4089	gap of unknown length
4089	5185	contig of 1096 bp in length
5185	5285	gap of unknown length
5285	6392	contig of 1107 bp in length
6392	6492	gap of unknown length
6492	7511	contig of 1019 bp in length
7511	7611	gap of unknown length
7611	9387	contig of 1776 bp in length
9387	9487	gap of unknown length
9487	10526	contig of 1039 bp in length
10526	10626	gap of unknown length
10626	12148	contig of 1522 bp in length
12148	12248	gap of unknown length
12248	13772	contig of 1524 bp in length
13772	13872	gap of unknown length
13872	14873	contig of 1101 bp in length
14873	15073	gap of unknown length
15073	15074	contig of 1831 bp in length
15074	16904	gap of unknown length
16904	17004	gap of unknown length
17004	18833	contig of 1829 bp in length
18833	18933	gap of unknown length
18933	20509	contig of 1576 bp in length
20509	20609	gap of unknown length
20609	21926	contig of 1317 bp in length
21926	22026	gap of unknown length
22026	24023	contig of 1997 bp in length
24023	24123	gap of unknown length
24123	25466	contig of 1523 bp in length
25466	25746	gap of unknown length
25746	27243	contig of 1497 bp in length
27243	27343	gap of unknown length
27343	28773	contig of 1430 bp in length
28773	28873	gap of unknown length
28873	30287	contig of 1414 bp in length
30287	30387	gap of unknown length
30387	32273	contig of 1866 bp in length
32273	32374	gap of unknown length
32374	34750	contig of 2377 bp in length
34750	34850	gap of unknown length
34850	37601	contig of 2751 bp in length
37601		gap of unknown length

37702	40012	contig of 2311 bp in length
40013	40112	gap of unknown length
40113	42937	contig of 2825 bp in length
42938	43037	gap of unknown length
43038	48102	contig of 5065 bp in length
48103	48202	gap of unknown length
48203	51825	contig of 3623 bp in length
51826	51925	gap of unknown length
51926	55645	contig of 3721 bp in length
55647	55746	gap of unknown length
55747	58157	contig of 2411 bp in length
58158	58257	gap of unknown length
58258	62954	contig of 4697 bp in length
62955	63055	gap of unknown length
63055	68502	contig of 5448 bp in length
68503	68602	gap of unknown length
68603	71952	contig of 3350 bp in length
71953	72052	gap of unknown length
72053	72505	contig of 4496 bp in length
72548	76648	gap of unknown length
76649	85400	contig of 8752 bp in length
85401	85500	gap of unknown length
85501	90053	contig of 4555 bp in length
90056	90155	gap of unknown length
90156	95604	contig of 5449 bp in length
95605	95704	gap of unknown length
95705	102981	contig of 7277 bp in length
102982	103081	gap of unknown length
103082	108599	contig of 5518 bp in length
108600	148669	gap of unknown length
148670	144262	contig of 5563 bp in length
144263	144363	gap of unknown length
144363	121717	contig of 7355 bp in length
121718	121817	gap of unknown length
121818	129537	contig of 7720 bp in length
129538	129637	gap of unknown length
129638	137014	contig of 7377 bp in length
137015	137114	gap of unknown length
137115	144344	contig of 7130 bp in length
144345	144424	gap of unknown length
144425	160413	contig of 16069 bp in length

[illegible]

Query Match	29.6%;	Score 80;	DB 2;	Length 160413;
Best Local Similarity	59.0%;	Pred. NO. 9e-05;		
Matches 128;	Conservative 0;	Mismatches 89;	Indels 0;	Gaps 0;

[illegible]

RESULT 5			
BC032803/c			
LOCUS	625 bp	mRNA	linear
BC032803			PRI 27-JUN-2002

DEFINITION	Homo sapiens, clone IMAGE:3865769, mRNA, partial cds.
ACCESSION	BC032803
VERSION	BC032803.1 GI:21619237
KEYWORDS	
SOURCE	human.

REFERENCE 1 (bases 1 to 625)

TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
not

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Screening: Stratagene, Inc.

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brook
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Maduro, Q. L., Mastello, C., Maskeri, B., Mastrian, S. D., McClosk
McDowell, J., Pearson, R., Stantropop, S., Thomas, P. J., Touchm

Young, A., Zhang, L.-H. and Green, E.D.

through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.infn.it>
 Series: IRAK Plate: 68 Row: b Column: 1.

Source

CDS

BASE COUNT	190 a	169 c	147 g	119 t
ORIGIN				

Query Match	29.48	Score	79.4	DB	9	Length	625
Best Local Similarity	65.58	Pred No.	0.00016				
Matches	116	Conservative	0	Mismatches	61	Indels	0
						Gaps	0

[illegible]

TITLE Direct Submission
JOURNAL Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 179601)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:20467523.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GLIV
Center clone name: CH230-156C8
----- Summary Statistics
Sequencing vector: Plasmid:
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 107997 bases at least Q40
Consensus quality: 114232 bases at least Q30
Consensus quality: 120314 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 84 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1196 1195: contig of 1195 bp in length
1296 1295: gap of unknown length
1296 2468: contig of 1173 bp in length
2469 2568: gap of unknown length
2569 3763: contig of 1195 bp in length
3764 3863: gap of unknown length
3864 5048: contig of 1185 bp in length
5049 5148: gap of unknown length
5149 6244: contig of 1096 bp in length
6245 6344: gap of unknown length
6345 7562: contig of 1218 bp in length
7563 7662: gap of unknown length
7663 8890: contig of 1228 bp in length
8891 8990: gap of unknown length
8991 10258: contig of 1268 bp in length
10259 10358: gap of unknown length
10359 11386: contig of 1028 bp in length
11387 11486: gap of unknown length
11487 12557: contig of 1071 bp in length
12558 12657: gap of unknown length
12659 14079: contig of 1422 bp in length
14080 14179: gap of unknown length
14180 15346: contig of 1167 bp in length
15347 15446: gap of unknown length
15447 16653: contig of 1207 bp in length
16654 16753: gap of unknown length
16754 17838: contig of 1085 bp in length
17839 17938: gap of unknown length
17939 19146: contig of 1208 bp in length
19147 19246: gap of unknown length
19247 20344: contig of 1098 bp in length
20345 20444: gap of unknown length
20445 21525: contig of 1081 bp in length
21526 21625: gap of unknown length
21626 22663: contig of 1038 bp in length
22664 22763: gap of unknown length

Query Match

22764 23897: contig of 1134 bp in length
23898 23997: gap of unknown length
23998 25011: contig of 1014 bp in length
25012 25111: gap of unknown length
25112 26444: contig of 1333 bp in length
26445 26544: gap of unknown length
26545 27620: contig of 1076 bp in length
27621 27720: gap of unknown length
27721 28770: contig of 1050 bp in length
28771 28870: gap of unknown length
28871 29951: contig of 1081 bp in length
29952 30052: gap of unknown length
30052 31220: contig of 1168 bp in length
31220 31320: gap of unknown length
31320 32966: contig of 1677 bp in length
32967 33096: gap of unknown length
33097 34103: contig of 1007 bp in length
34104 34203: gap of unknown length
34204 35225: contig of 1022 bp in length
35226 35325: gap of unknown length
35326 36948: contig of 1623 bp in length
36949 37048: gap of unknown length
37049 38400: contig of 1352 bp in length
38401 38500: gap of unknown length
38501 40784: contig of 2284 bp in length
40785 40884: gap of unknown length
40885 42959: contig of 2075 bp in length
42960 43059: gap of unknown length
43060 44535: contig of 1496 bp in length
44536 44655: gap of unknown length
44656 46911: contig of 2256 bp in length
46912 47011: gap of unknown length
47012 48011: contig of 1000 bp in length
48012 48111: gap of unknown length
48112 49469: contig of 1358 bp in length
49470 49569: gap of unknown length
49570 50778: contig of 1209 bp in length
50779 50878: gap of unknown length
50879 52371: contig of 1493 bp in length
52372 52471: gap of unknown length
52472 53583: contig of 1112 bp in length
53584 53683: gap of unknown length
53684 55593: contig of 1910 bp in length
55594 55693: gap of unknown length
55694 57682: contig of 1989 bp in length
57683 57782: gap of unknown length
57783 59073: contig of 1291 bp in length
59074 59173: gap of unknown length
59174 60451: contig of 1278 bp in length
60452 60551: gap of unknown length
60552 62245: contig of 1694 bp in length
62246 62345: gap of unknown length
62346 64542: contig of 2197 bp in length
64543 64642: gap of unknown length
64643 65836: contig of 1194 bp in length
65837 65936: gap of unknown length
65937 67056: contig of 1120 bp in length
67057 67156: gap of unknown length
67157 68772: contig of 1616 bp in length
68773 68872: gap of unknown length
68873 70285: contig of 1413 bp in length
70286 70385: gap of unknown length
70386 72215: contig of 1830 bp in length
72216 72315: gap of unknown length
72316 73774: contig of 1458 bp in length
73775 73873: gap of unknown length
73874 75182: contig of 1309 bp in length
75183 75282: gap of unknown length
75283 77308: contig of 2026 bp in length
77309 77408: gap of unknown length
77409 78877: contig of 1469 bp in length

28.5% Score 77; DB 2; Length 179601;

REFERENCE
AUTHORS
TITLE
JOURNAL

Enkayayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1705)
Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CNA Library Preparation: Life Technologies, Inc.
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nhgri.nih.gov
Ahler, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., McGoss, J.R.,
Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stathitop, S., Thomas, P. J., Touchman, J.W.,
Tsurgren, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/INL at: <http://image.lnl.gov>
Series: IRAK Plate: 62 Row: 3 Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.

FEATURES
SOURCE

polyA-site	1537	/gene="DKFZp667L2116"
BASE COUNT	540 a	300 c 270 g 511 t
ORIGIN		

Query Match	28.1%	Score 76:	DB 9:	Length 1621;
Best Local Similarity	73.5%	Pred. No. 0.0006;		
Matches 97:	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;

[illegible]

QY	127	AGGGCGGGGAG	138
Db	1500	AGCATGCAAAAG	1489

RESULT 13					
BC032249/c					
LOCUS	BC032249	1705 bp	mRNA	linear	PRI 27-JUN-2002
DEFINITION	Homo sapiens, clone MGC:40072 IMAGE:51217556, mRNA, complete cds.				

VERSION	BC032249.1	GI:21619009
KEYWORDS	MGC.	
SOURCE	human.	
ORGANISM	Homo sapiens	

```

/codon_start=-1
/product="unknown (protein for MGC:40072)"
/protein_id="AAH32249.1"
/db_xref="GI:21619010"
/translation="MEFGLSWFLVAILKQVCEVQLVESGGGVYRRPGSLRLSCAAS
GFNFDYSGASVAVRQADPKGLEWSSILMMNGSSITPAASVGRFTLISDNKNSLYLDM
NSLRVEDTALYCAQADPTKLTCSGSGCYMDWGKCTVYSASPTSPKRPFLSL
SPQDGNVYIACIQGFPPEQPLSYMSESGGCVTAANPPSDASDILYTSQULL
PATQCLAGKSVYTHVKHYITNPSSDYVPCVTPSPPIPPSPSTPDSQCPRLSLA
RPALEDLLGSEANLITGLLRDASVATPTWTPSSKSAVQGGPDDILGCVSVSSV
LPCAEFWMHNGKTFETCAAPSEKTPITALSLSGNFREYVHLLSEELANLEYL
TFLCLARGSPKDVILWMLQSGOELPREKILTVMASREDSQTTTFVSTSLRAAED
WKKGDFEFCMWGHEALPLATFOKTRIDRLACKPHTVANSVYMALEDVGCY"

```

Query Match	28.1%	Score 76	DB 9	Length 1705
Best Local Similarity	73.5%	Pred. No.	0 00059	
Matches 97	Conservative	0	Mismatches 35	Indels 0
				Gaps 0

[illegible]

QY 127 AGGCGCGGAG 138
Db 1561 CAGTACGAGTGT 1550

RESULT 14
AC106085
LOCUS AC106085
DEFINITION Rattus norvegicus clone CH230-125G16, *** SEQUENCING IN PROGRESS
AC106085.2 GI:21729541
VERSION AC106085
KEYWORDS HTG; HNGS; PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 186866)
AUTHORS Muzny D.M., Adams C., Adlo-Oduola B., Ali-osman F.R., Allen C., Alsbrooks S.L., Amaratunga H.C., Are J.R., Ayele M., Banks T., Barbata J., Benton J., Blmage K., Blankenburg K., Bonin D., Bouck J., Bowle S., Brileva M., Brown E., Brown M., Bryant N.P., Buhay C., Burch P., Burkett C., Burrell K.L., Byrd N.C., Carron T.F., Carter M., Cavazos S.R., Chacko J., Chavez D., Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos C., Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R., Davila M.L., Davis C., Davy-Carroll L., Dederich D.A., Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H., Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J., Earnhart C., Edgar D., Edwards C.C., Elhaj C., Escotto M., Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P., Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R., Gorrell J.H., Guevara W., Gunaratne P., Hale S., Hamilton K., Harris C., Harris K., Hart M., Havlak P., Hawes A., Hernandez J., Hernandez O., Hodgson A., Hognes M., Holloway C., Hollins B., Homsi F., Howard S., Huber J., Huliy S., Hume J., Jackson L.E., Jacobson B., Jia Y., Johnson R., Jolivet S., Joudah S., Karlsson E., Kelly S., Khan U., King L., Kovach J., Kovar C., Kratochvil J., Kureshi A., Landry N., Leal B., Lewis L.C., Lewis L., Li J., Li Z., Lichtarge O., Lieu C., Liu J., Liu W., Louisedge H., Lozada R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J., Maheshwari M., Mapua P., Martin R., Martindale A., Martinez E., Massey E., Mawhney E., McLeod M.P., Meador M., Mel G., Metker M., Miner G., Miner Z., Mitchell T., Mohabbat K., Morgan M., Morris S., Moser G., Neal D., Newton J., Newton N., Nguyen A., Nguyen G., Nguyen N., Nickerson E., Nwoekenwo S., Ogun M., Okwuonu G., Oragunye N., Oviedo R., Pace A., Payton B., Peery J., Perez L., Peters L., Pickens R., Primus E., Pu L.L., Quiles M., Ren Y., Rives M., Rojas A., Rojubokan I., Rolfe M., Ruiz S., Savery G., Scherer S., Scott G., Shen H., Shoshitari N., Sisson I., Sodergren E., Sonalke T., Sparks A., Stanley H., Stone H., Sutton A., Svatek A., Tabor P., Tamerisa A., Tamerisa K., Tang H., Tansey J., Taylor C., Taylor T., Telford B., Thomas N., Thomas S., Usmani K., Vasquez L., Vera V., Villalón D., Vinton R., Wang O., Wang S., Ward-Moore S., Warren R., Washington C., Watlington S., Williams G., Williamson A., Wlecczyk R., Wooden S., Worley K., Wu C., Wu Y., Wu Y.F., Zhou J., Zortilla S., Nelson D., Weinstein G., and Gibbs R.

TITLE AC106085
JOURNAL
REFERENCE 2 (bases 1 to 186866)
AUTHORS Worley K.C.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 186866)
AUTHORS Worley K.C.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 11, 2002 this sequence version replaced gi:18138600.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHQ
Center clone name: CH230-125G16
----- Summary Statistics
Sequencing vector: M13
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 110546 bases at least Q40
Consensus quality: 117272 bases at least Q30
Consensus quality: 123085 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 76 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 1343
* 1442: contig of 1342 bp in length
* 1443
* 2787: contig of 1345 bp in length
* 2788
* 2888: gap of unknown length
* 2888
* 4594: contig of 1707 bp in length
* 4595
* 4694: gap of unknown length
* 4695
* 6283: contig of 1588 bp in length
* 6283
* 6382: gap of unknown length
* 6383
* 7467: contig of 1084 bp in length
* 7467
* 7566: gap of unknown length
* 7567
* 8845: contig of 1279 bp in length
* 8846
* 8945: gap of unknown length
* 8946
* 10100: contig of 1155 bp in length
* 10101
* 10200: gap of unknown length
* 10201
* 11531: contig of 1331 bp in length
* 11532
* 11631: gap of unknown length
* 11632
* 13301: contig of 1670 bp in length
* 13302
* 13401: gap of unknown length
* 13402
* 14538: contig of 1137 bp in length
* 14539
* 14638: gap of unknown length
* 14639
* 16370: contig of 1732 bp in length
* 16371
* 16470: gap of unknown length
* 16471
* 17842: contig of 1372 bp in length
* 17843
* 17942: gap of unknown length
* 17943
* 19180: contig of 1238 bp in length
* 19181
* 19280: gap of unknown length
* 19281
* 20625: contig of 1345 bp in length
* 20626
* 20725: gap of unknown length
* 20726
* 22270: contig of 1545 bp in length
* 22271
* 22370: gap of unknown length
* 22371
* 23905: contig of 1535 bp in length
* 23906
* 24005: gap of unknown length
* 24006
* 25343: contig of 1338 bp in length
* 25344
* 25443: gap of unknown length
* 25444
* 26388: contig of 1195 bp in length
* 26389
* 26738: gap of unknown length
* 26739
* 28065: contig of 1327 bp in length
* 28066
* 28165: gap of unknown length
* 28166
* 29652: contig of 1487 bp in length
* 29653
* 29752: gap of unknown length
* 29753
* 31143: contig of 1391 bp in length
* 31144
* 31243: gap of unknown length
* 31244
* 32321: contig of 1078 bp in length
* 32322
* 32421: gap of unknown length
* 32422
* 33527: contig of 1106 bp in length
* 33528
* 33627: gap of unknown length

Claim 1, Page 70; 71pp; English.

The sequences given in AAH43636-47 represent Stomach Cancer Specific Genes (SSG's). These polynucleotides were isolated using a PCR based subtractive hybridization method on subtracted libraries which were generated for stomach. The CDNA libraries contained expressed sequence tags (EST's) from genes that are stomach cancer specific or are upregulated in stomach. These polynucleotides and the corresponding encoded polypeptides are useful for diagnosing, monitoring, staging, imaging or treating cancer, particularly stomach cancer.

Sequence 270 BP; 49 A; 57 C; 75 G; 87 T; 2 other;

Query Match 99.3%; Score 268; DB 22; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 ACAACCTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTAAATTTT 60
1 ACAACCTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTAAATTTT 60
61 TTTTTTTTTTTTTTTTTTTCCCGTGGAGCACACGTCATTTGGGGGCCAGTCTCCGG 120
61 TTTTTTTTTTTTTTTTCCCGCTGGAGCACACGTCATTTGGGGGCCAGTCTCCGG 120
121 GGGACACGAGGGCGGGAGGGGGGTGGAGCAGGGGCGAAGCCCGACGAGACGGGGGGG 180
121 GGGACACGAGGGCGGGAGGGGGGTGGAGCAGGGGCGAAGCCCGACGAGACGGGGGGG 180
181 ACACACAGGCGCAAAAGGGTGGTCCCGCTGTGGGAAATGTGTACCCGCGCCACAAATTC 240
181 ACACACAGGCGCAAAAGGGTGGTCCCGCTGTGGGAAATGTGTACCCGCGCCACAAATTC 240
241 CCCACACAAATTAACAGACAACTCANTCT 269
241 CCCACACAAATTAACAGACAACTCANTCT 269

RESULT 2
AAC85567/C
ID AAC85567 standard; cDNA: 2761 BP.
AAC85567;
04-JUN-2001 (first entry)
cDNA encoding CDIF-27, Incyte ID No. 2573955CB1.
Human: cell differentiation; CDIF: agonist; antagonist; epilepsy;
cell proliferation; Alzheimer's disease; schizophrenia disorder;
arteriosclerosis; cancer; atherosclerosis; diabetes mellitus; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 175..1767
FT /*tag= a
FT /product= "CDIF-27"
XX MO200119860-A2.
XX 22-MAR-2001.
XX 14-SEP-2000; 2000MO-US25435.
XX 15-SEP-1999; 99US-0154140.
XX 06-DEC-1999; 99US-0169155.
XX (INCYTE) INCYTE GENOMICS INC.
XX Tang YT, Hillman JL, Yue H, Reddy R, Lal P, Shah P, Azimzai Y;
XX Baughn MR, Lu DAM, Bandman O, Shih LL, Patterson C;

DR		WPI: 2001-211447/21.
DR	P-PsDB; AAB47145.	
PT	Isolated polypeptides and polynucleotides involved in cell	
PT	differentiation are used for treatment, prevention and diagnosis of	
PT	cell proliferative, developmental and neurological disorders e.g.	
PT	cancer and Alzheimer's disease -	
PS	Claim 5; Page 136-137; 137pp; English.	
XX		
CC	The sequences given in AAC8545-72 encode human polypeptides involved	
CC	in cell differentiation (CDIF). CDIF polypeptides and agonists of	
CC	these are used to treat a disease or condition associated with	
CC	decreased expression of functional CDIF. An antagonist of CDIF is	
CC	used to treat a disease or condition associated with over expression	
CC	of functional CDIF. CDIF polypeptides may be used for the treatment,	
CC	prevention and diagnosis of cell proliferative, developmental and	
CC	neurological disorders, such as Alzheimer's disease, schizophrenia	
CC	disorders, arteriosclerosis, cancer, atherosclerosis, diabetes mellitus	
CC	and epilepsy. The CDIF-27 sequence is similar to auxin-responsive GH3	
CC	protein. The CDIF-27 coding sequence maps to chromosome 1 within	
CC	the interval from 22.9 to 39.9 centimorgans, and to chromosome 3 within	
CC	the interval from 30.9 to 43.0 centimorgans.	
SO	Sequence 2761 BP; 556 A; 815 C; 855 G; 535 T; 0 other:	
Query Match	30.2%; Score 81.6; DB 22;	Length 2761;
Best Local Similarity	73.8%; Pred. No. 2.4e-05;	
Matches 118; Conservative	0; Mismatches 39; Indels	3; Gaps 1;
OY	7	TTTTTTTTTTTTTTTTTTTTTTTTTTCCTTTTAAATTTTTTTTTT
Db	2457	TTTTTTTTTTTTTTTTTTTTTTTTT
OY	67	TTTTTTTTTCCCCTGGAGCACACGTCATTGTGGGCCAGTCTCCCGGGAGC
Db	2397	TTTTTTTTTTTTTCTCGGTGCAGAGAGTTATTGTGGAGCCA---TCCAGGAAGCCC
OY	127	AGGCGCCGGAGGGGGGTGAGCAGAGGGCGCAACCCCC
Db	2340	AAGCGGGGGAGTGGGGAAGAAGAGGAGGAGACC
RESULT 3		
ABV34102		
ID	ABV34102 standard; cDNA; 462 BP.	
XX		
AC	ABV34102;	
XX		
DE	16-SEP-2002 (first entry)	
XX		
Human.prostate expression marker cDNA 34093.		
XX		
Human; prostate cancer; cytosstatic; carcinogen; pharmacodynamic marker;		
KW	pharmacogenomic marker; gene; ss.	
XX		
Homo sapiens.		
OS		
MO200160860-A2.		
XX		
PD	23-AUG-2001.	
XX		
PF	20-FEB-2001; 2001WO-USO5171.	
XX		
PR	17-FEB-2000; 2000US-183319P.	
PR	16-MAR-2000; 2000US-189862P.	
PR	25-MAY-2000; 2000US-207454P.	
PR	09-JUN-2000; 2000US-211314P.	
PR	18-JUL-2000; 2000US-215007P.	
PR	13-DEC-2000; 2000US-255281P.	
XX		
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	

Query	Subject	Score	Length	Matches	Mismatches	Indels	Gaps
1	ABV42965	30.0%	462	129	0	80	0
2	ABV42965	30.0%	462	129	0	80	0
3	ABV42965	30.0%	462	129	0	80	0
4	ABV42965	30.0%	462	129	0	80	0
5	ABV42965	30.0%	462	129	0	80	0
6	ABV42965	30.0%	462	129	0	80	0
7	ABV42965	30.0%	462	129	0	80	0
8	ABV42965	30.0%	462	129	0	80	0
9	ABV42965	30.0%	462	129	0	80	0
10	ABV42965	30.0%	462	129	0	80	0
11	ABV42965	30.0%	462	129	0	80	0
12	ABV42965	30.0%	462	129	0	80	0
13	ABV42965	30.0%	462	129	0	80	0
14	ABV42965	30.0%	462	129	0	80	0
15	ABV42965	30.0%	462	129	0	80	0
16	ABV42965	30.0%	462	129	0	80	0
17	ABV42965	30.0%	462	129	0	80	0
18	ABV42965	30.0%	462	129	0	80	0
19	ABV42965	30.0%	462	129	0	80	0
20	ABV42965	30.0%	462	129	0	80	0
21	ABV42965	30.0%	462	129	0	80	0
22	ABV42965	30.0%	462	129	0	80	0
23	ABV42965	30.0%	462	129	0	80	0
24	ABV42965	30.0%	462	129	0	80	0
25	ABV42965	30.0%	462	129	0	80	0
26	ABV42965	30.0%	462	129	0	80	0
27	ABV42965	30.0%	462	129	0	80	0
28	ABV42965	30.0%	462	129	0	80	0
29	ABV42965	30.0%	462	129	0	80	0
30	ABV42965	30.0%	462	129	0	80	0
31	ABV42965	30.0%	462	129	0	80	0
32	ABV42965	30.0%	462	129	0	80	0
33	ABV42965	30.0%	462	129	0	80	0
34	ABV42965	30.0%	462	129	0	80	0
35	ABV42965	30.0%	462	129	0	80	0
36	ABV42965	30.0%	462	129	0	80	0
37	ABV42965	30.0%	462	129	0	80	0
38	ABV42965	30.0%	462	129	0	80	0
39	ABV42965	30.0%	462	129	0	80	0
40	ABV42965	30.0%	462	129	0	80	0
41	ABV42965	30.0%	462	129	0	80	0
42	ABV42965	30.0%	462	129	0	80	0
43	ABV42965	30.0%	462	129	0	80	0
44	ABV42965	30.0%	462	129	0	80	0
45	ABV42965	30.0%	462	129	0	80	0
46	ABV42965	30.0%	462	129	0	80	0
47	ABV42965	30.0%	462	129	0	80	0
48	ABV42965	30.0%	462	129	0	80	0
49	ABV42965	30.0%	462	129	0	80	0
50	ABV42965	30.0%	462	129	0	80	0
51	ABV42965	30.0%	462	129	0	80	0
52	ABV42965	30.0%	462	1			

PR	09-JUN-2000; 2000US-211314P.
PR	18-JUL-2000; 2000US-21907P.
PR	13-DEC-2000; 2000US-235281P.
XX	
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	
PI	Schlegel R, Endege WO, Monahan JE;
XX	
DR	WPI; 2001-662795/76.
XX	
PT	Novel isolated nucleic acid molecule associated with cancerous state of
PT	prostate cells and correlating with presence of prostate cancer, useful
PT	for detecting presence of prostate cancer, stage of prostate cancer -
XX	
PS	Claim 1; Page 8583; 11750pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC	specification or its complement. (I) is useful for:
CC	(a) assessing whether a patient is afflicted with prostate cancer;
CC	(b) monitoring the progression of prostate cancer in a patient;
CC	(c) assessing the efficacy of a test compound to inhibit prostate
CC	cancer in a patient;
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC	in a patient;
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;
CC	(f) assessing the prostate cell carcinogenic potential of a compound;
CC	(g) determining whether prostate cancer has metastasized in a patient;
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a
CC	patient;
CC	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX	
SQ	Sequence 462 BP; 103 A; 81 C; 135 G; 143 T; 0 other;
	Query Match 30.0%; Score 81; DB: 23; Length 462;
	Best Local Similarity 61.7%; Pred. No. 3e-05;
	Matches 129; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY	7 TTTTTTTTTTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTAAATTTTTTTTTT 66
Db	
	99 TTTTTTTTTTTTTTTTTTTTTTTTTTTT
	158
QY	67 TTTTTTTTTTCCCGGAGACACAGGTCATTGGGGGCGAGTCTCCGGGGAGC 126
Db	
	159 TTTTTTTTTTTTTTTTAAAAAACCCGGGAACCGGGGCGGTAAAAAAAAGGGAGC 218
QY	127 AGGGCGCGGAGGGGGGCGTGGAGAGGGGGGACGCCCCAGAAACGGGGCGACACAC 186
Db	
	219 CCGCGGGGGGGGGGGGGAATAAATTAATGAACCCCGCACCGGGGGGGGGC 278
QY	187 AGCGACAAAGGTCGTCCTGTGGGG 215
Db	
	279 CCGCCCCCAATTTTGGTCCTTAAGGG 307
RESULT 5	
ABV12980	
ID	ABV12980 standard; cDNA: 629 BP.
XX	
AC	ABV12980;
XX	
DT	13-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker CDNA 12971.
XX	
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW	pharmacogenomic marker; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200160860-A2.
XX	
DD	23-AUG-2001.

XX		20-FEB-2001; 2001MO-US05171.
Pf		
XX		
PR	17-FEB-2000; 2000US-183319P.	
PR	16-MAR-2000; 2000US-189862P.	
PR	25-MAY-2000; 2000US-207454P.	
PR	09-JUN-2000; 2000US-211314P.	
PR	18-JUL-2000; 2000US-219007P.	
PR	13-DEC-2000; 2000US-255281P.	
XX		
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
PI	Schlegel R, Endege WO, Monahan JE;	
DR	WPI: 2001-662795/76.	
XX		
PT	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -	
PT		
XX		
PS	Claim 1; Page 2141; 11750pp; English.	
CC	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABY00010-ABV62213) of the specification or its complement. (I) is useful for:	
CC	(a) assessing whether a patient is afflicted with prostate cancer;	
CC	(b) monitoring the progression of prostate cancer in a patient;	
CC	(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;	
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;	
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;	
CC	(f) assessing the prostate cell carcinogenic potential of a compound;	
CC	(g) determining whether prostate cancer has metastasized in a patient;	
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a patient;	
CC	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.	
SO	Sequence 629 BP; 165 A; 110 C; 194 G; 157 T; 3 other;	
	Query Match 30.0%; Score 81; DB 23; Length 629;	
	Best Local Similarity 61.7%; Pred. NO. 3e-05;	
	Matches 129; Conservative 0; Mismatches 80; Indels 0; Gaps 0	
OY	7 TTTTCTTTTTTTTTTTTTTTTTTTTTTCCTTTTTTTTTTTTTTAATTTTTTTTTTTT 66	
Db	51 TTTTCTT 110	
OY	67 TTTTCTTTTTCCCCCGTGAGCACACGCTCAATTGGGGGCCAGGTCTCCGGGGGACC 126	
Db	111 TTTTCTTTTTTTTTTTTTTTAAATAAACCCCGGGAACCCGGGCGGTAAATAAAGGGACC 170	
OY	127 AGGGCGCGGAGGGGGGGGTGAGCAGCAGGGGGACACGCCCCAGAGAAGCGGGCGGCACAC 186	
Db	171 CCOCGGGGGGGGGGGGGGGAAAAAACGTTATGAACCCGCCACCGGGGGGGGGGCC 230	
OY	187 AGGAGCAAAGGCTGGTCCCGTGNGGG 215	
Db	231 CGGCCCAATTTTGTGTCCTTAAGGG 259	
RESULT 6		
AAI88874/c		
ID	AAI88874 standard; cDNA: 758 BP.	
AI88874:		
XX		
DT	06-NOV-2001 (first entry)	
XX		
DE	Human polynucleotide seq ID NO 8934.	
XX		
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; hematopoiesis;	

[illegible]

DE	Human polynucleotide SEQ ID NO 8935.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KM	nervous system disorders; arthritis; inflammation; ss.
OS	Homo sapiens.
PN	WO200164835-A2.
PD	07-SEP-2001.
PE	26-FEB-2001; 2001WO-US04927.
PR	28-FEB-2000; 2000US-0515126.
PR	18-MAY-2000; 2000US-0577409.
PA	(HYSE-) HYSEQ INC.
PI	Tang YT, Liu C, Drmanac RT;
DR	WPI: 2001-514838/56.
P	P-PSDB; AA008944.
PT	Isolated nucleic acids and polypeptides, useful for preventing
PT	diagnosing and treating e.g. leukaemia, inflammation and immune
PT	disorders -
PS	Claim 1; SEQ ID NO 8935; 1399pp + Sequence Listing: English.
XX	
CC	The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC	cyclokin, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapy. The polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activating and
CC	activin/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC	inflammation.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 767 BP; 227 A; 117 C; 95 G; 225 T; 103 other;
Query Match	29.3%; Score 79; DB 22; Length 767;
Best Local Similarity	64.5%; Pred. No. 6.5e-05;
Matches 118; Conservative	0; Mismatches 65; Indels 0; Gaps 0
OY	1 ACAAGCTTTTTTTTTTTTTTTTTTTTTTTTTCCTTTTTTTTTTTTTTTAATTTT 60
OY	.267 AAAAATTT 208
OY	61 TTTTITTTTTTTTTTCCCCTGGGAGCACACGTCATTGCGGCCAGTCTCCCG 120
OY	207 TTTTITTTTTTTTTTGCGCGCCACATCAGCTTTATTCAAAAGACACGCGGTGTC 148
OY	121 GGAGCAGAGCGCGGGAGGGGGGAGGCAGAGGGCAACACCCTCAGGAACGGGGGGG 180
OY	147 AGGAAGGGAGAGAGGGGCTGGGGGAGAGCCCAAGGGGCAAGAAGCATGGCCACCGAGCT 88
OY	181 ACA 183
OY	87 CCA 85
Db	
RESULT 8	
TALE1014	
ID	AA10104 standard; cDNA; 373 BP.
XX	

AC			AL10104;			
XX						
DT	07-DEC-2001	(first entry)				
XX						
DE		Human breast cancer expressed polynucleotide 2561.				
XX						
KW		Human; breast cancer; cell marker; cytostatic; ss.				
XX						
OS		Homo sapiens.				
XX						
PN		MO200151628-A2.				
PD						
XX		19-JUL-2001.				
PF						
PE		10-JAN-2001; 2001WO-US00798.				
XX						
PR		14-JAN-2000; 2000US-0176077.				
PR		14-MAR-2000; 2000US-0189167.				
PR		24-MAR-2000; 2000US-0192099.				
PR		29-MAR-2000; 2000US-0193480.				
PR		15-MAY-2000; 2000US-0205230.				
PR		09-JUN-2000; 2000US-0211315.				
PR		25-JUL-2000; 2000US-0220534.				
PA						
XX		(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.				
PI	Lillie J, Xu Y, Wang Y, Steinhann K;					
XX						
DR	WPI: 2001-451856/48.					
PT		New peptide useful as a marker for the diagnosis of breast cancer -				
XX						
PS		Claim 1: Page 486-487; 3695pp; English.				
XX						
CC		The invention relates to human breast cancer expressed polynucleotides				
CC		(AAH07544-AAH26789) and methods of assessing whether a patient is				
CC		afflicted with breast cancer by examining the correlation between the				
CC		expression of certain markers and the cancerous state of breast cells.				
CC		The polynucleotides and encoded polypeptides are potential markers for				
CC		detecting, diagnosing, monitoring, characterizing treating and				
CC		potentially preventing breast cancer. The polynucleotides and encoded				
CC		polypeptides are also useful for isolating compounds with cytostatic				
CC		activity.				
SQ		Sequence 373 BP; 73 A; 62 C; 63 G; 121 T; 54 other:				
	Query Match	28.7%; Score 77.4; DB 22; Length 373;				
	Best Local Similarity	56.3%; Pred. No. 0.00012;				
	Matches	111; Conservative 0; Mismatches 86; Indels 0; Gaps 0;				
OY	6 CTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTCCTTTTTTTTTTTTAATTTTTTTTTTTT	65				
Dd						
	74 CTTTCTT	133				
OY	66 TTTTCTTTTTTCCCCCGGAGGCACACGGCATTGTGGGGGCCAGGCTCCC GGCGAG	125				
Dd						
	134 TTTTCTTTTTTGSCCCCCCNCCANNTTNAATAAANGGNAAAAGNNTNTNNAAAA	193				
OY	126 CAGGGCGGGAAGAAGGGGGGTGTGAGCACAGGGGGCAACGCCCCAGAACGGGGCGACACA	185				
Dd	124 AAAGGGGGGGGGGCAAGCAACCAAAAANCCCCCAAACCAGGGGGCNTNTNGMAAMAN	253				
OY	186 CAGGCGACAAAGGCTGG 202					
Dd	254 NAGCMGNCNMAGNMGNGG 270					
RESULT 9						
AAH69374						
ID	AAH69374 standard; CDNA: 440 BP.					
XX						
MC	AAH69374;					
XX						

[illegible]

XV	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XW	pharmacogenomic marker; gene; ss.
KM	Homo sapiens.
OS	WO200160860-A2.
PN	23-AUG-2001.
XX	20-FEB-2001; 2001WO-US05171.
PF	17-FEB-2000; 2000US-183319P.
XX	16-MAR-2000; 2000US-189862P.
PR	25-MAY-2000; 2000US-207454P.
PR	09-JUN-2000; 2000US-211314P.
PR	18-JUL-2000; 2000US-219007P.
PR	13-DEC-2000; 2000US-255281P.
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA	Schlegel R, Endege WO, Monahan JE;
XX	WPI, 2001-662795/76.
DR	Novel isolated nucleic acid molecule associated with cancerous state of
PT	prostate cells and correlating with presence of prostate cancer, useful
PJ	for detecting presence of prostate cancer, stage of prostate cancer -
XX	Claim 1; Page 10503; 11750pp; English.
PS	The invention relates to an isolated nucleic acid molecule (I) comprising
XX	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC	specificiation or its complement, (I) is useful for:
CC	(a) assessing whether a patient is afflicted with prostate cancer;
CC	(b) monitoring the progression of prostate cancer in a patient;
CC	(c) assessing the efficacy of a test compound to inhibit prostate
CC	cancer in a patient;
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC	in a patient;
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;
CC	(f) assessing the prostate cell carcinogenic potential of a compound;
CC	(g) determining whether prostate cancer has metastasized in a patient;
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a
CC	patient;
CC	(i) is also useful as a pharmacodynamic or pharmacogenomic marker.
CC	Sequence 453 BP; 130 A; 105 C; 105 G; 110 T; 3 other;
SQ	
Query Match	28.1%; Score 76; DB 23; Length 453;
Best Local Similarity	76.5%; Pred. No. 0.00021;
Matches 91; Conservative	0; Mismatches 28; Indels 0; Gaps 0
OY	7 TTTTTCCTTTTTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTTTTTAAATTTTTTTTTT 66
Db	120 TTTTTCCTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 61
OY	67 TTTTTCCTCCCCCGTGAGACACGCGTCAATTGGGGCCAGGTCTCCGGGGGAG 125
Db	60 TTTTTCCTTTTTTGCCTGGGGAGCCCGCGTAAATTATNCACAAGTACNCGAAGGGG 2
RESULT 11	
ABV15289	
ID	ABV15289 standard; cDNA; 461 BP.
XX	
AC	ABV15289;
XX	
DT	13-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker CDNA 15280.
XX	
XW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KM		pharmacogenomic marker; gene; ss
XX		
OS	Homo sapiens.	
XX		
PN	WO200160860-A2.	
XX		
PD	23-AUG-2001.	
XX		
PE	20-FEB-2001; 2001WO-USO5171.	
XX		
PR	17-FEB-2000; 2000US-183319P.	
PR	16-MAR-2000; 2000US-189862P.	
PR	25-MAY-2000; 2000US-207454P.	
PR	09-JUN-2000; 2000US-211314P.	
PR	18-JUL-2000; 2000US-219007P.	
PR	13-DEC-2000; 2000US-255281P.	
XX		
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX		
PI	Schlegel R, Endege WO, Monahan JE;	
DR	WPI; 2001-662795/76.	
XX		
PT	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -	
PT		
XX	Claim 1; Page 2564; 11750pp; English.	
PS		
CC	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:	
CC	(a) assessing whether a patient is afflicted with prostate cancer;	
CC	(b) monitoring the progression of prostate cancer in a patient;	
CC	(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;	
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;	
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;	
CC	(f) assessing the prostate cell carcinogenic potential of a compound;	
CC	(g) determining whether prostate cancer has metastasized in a patient;	
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a patient;	
CC	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.	
CC		
XX		
SQ	Sequence 461 BP; 70 A; 146 C; 113 G; 132 T; 0 other;	
	Query Match 27.6%; Score 74.6; DB 23; Length 461;	
	Best Local Similarity 59.8%; Pred. No. 0.00035;	
	Matches 125; Conservative 0; Mismatches 84; Indels 0; Gaps 0	
OY	7 TTTTTCCTTTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTTAATTTTTTTTTTTT 66	
Dd	22 TTTTTCCTTTAATT 81	
OY	67 TTTTTCCTTTCCCGGTGGAGACACAGGTCATTGCGGCCAGCTCCTCCGGGGAGC 126	
Dd	82 TTTTTCCTTTTAAAGGGTAACCCCCAACCCCTTTTAAACCCTGGGGGCCCCCCGA 141	
OY	127 AGGCGCGGGAGGGGGGTGAGACAGGGGCAACGCCCCAGACACGGGGGCACACAC 186	
Dd	142 AGGGGGGCGCTTGGGAGAGGGAATAACGGGGAAACCCCCACACTTTTCCAAAGGGGG 201	
OY	187 AGCGACAAGAAGGTGGGTCCCGTGAGG 215	
Dd	202 GGCGCAAAAAAGAGATTCCCTAGGGG 230	
RESULT 12		
AAQ35199/c		
ID	AAQ35199 standard; DNA; 1541 BP.	
AC	AAQ35199;	

```

XX      07-JUN-1993      (first entry)
DE
XX      ppcDHP23 coding sequence.
DE
XX
XX      Polypeptide; dehydropeptidase-1; DHP-1; activity,. carbapenem;
KM      antibiotic, ss.
KW
XX      Synthetic.
OS
XX      Key
FH      Location/Qualifiers
FT      CDS                120..1349
FT                                     /*tag= a
FT      sig_peptide        120..167
FT                                     /*tag= b
FT      mat_peptide        168..1346
FT                                     /*tag= c
XX
XX      JP05003790-A.
EN
XX
XX      14-JAN-1993.
PD
XX
XX      18-APR-1991;    91JP-0115493.
PE
XX
XX      19-APR-1990;    90JP-0103962.
PR
XX
XX      (FUJII ) FUJISAWA PHARM CO LTD.
PA
XX
XX      WPI: 1993-054800/07.
DR
XX      P-PSDB: MAR30823.
DR
XX
XX      Poly:peptide having dehydro:peptidase-1 enzyme activity - is
PT      physiologically active and reacts with carba:penem antibiotics
XX
XX      Disclosure; Fig 3-5; 25pp; Japanese.
XX
CC      The sequences given in AA035198-201 encode polypeptides which have
CC      dehydropeptidase-1 (DHP-1) enzyme activity. DHP-1 is a
CC      physiologically active substance which reacts with carbapenem
CC      antibiotics.
XX
SQ      Sequence 1541 BP; 339 A; 489 C; 471 G; 242 T; 0 other:

Query Match          27.6%; Score 74.6; DB 14; Length 1541;
Best Local Similarity 71.5%; Pred.No.0.00035;
Matches   98; Conservative   0; Mismatches   39; Indels   0; Gaps   0;

QY      7 TTTTTCCTTTTTTTTTTTTTTTTTTTCCTTTTTCCTTTTTTTTTTTAAATTTTTTTTTTTT 66
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1535 TTTTTCCTTTTTTTTTTTTTTTTTTTCCTTTTTCCTTTTTTTTTTTAAATTTTTTTTTTTT 1476

QY      67 TTTTTCCTTTCCCCCGTGAGCACAACGTCATTGTGGGGGCCAGGTCACCGGGGAGC 126
       ||| ||||| ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      1475 TTTTTCCTTTTTCGAAGTCGTGCATCCTTTATTGAGGTCGCCAGGCGCCCTCCGGAGC 1416

QY      127 AGGGCGCGGAGGAGGGG 143
       ||| | | | | | | |
Db      1415 CGGGCGCCGTCACAGG 1399

RESULT 13
ID      AAL23504 standard; CDNA; 758 BP.
XX
XX      AAL23504;
AC
XX
DT      07-DEC-2001 (first entry)
XX
DE      Human breast cancer expressed polynucleotide 15961.
XX
KW      Human; breast cancer; cell marker; cytostatic; ss.
XX
OS      Homo sapiens.
```

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XX PN WO200151628-A2.
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XX XX
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PD PD 19-JUL-2001.
```

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XX PF
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PE PE 10-JAN-2001; 2001WO-US00798.
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XX PR
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PR PR 14-JAN-2000; 2000US-0176077.
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PR PR 14-MAR-2000; 2000US-0189167.
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PR PR 24-MAR-2000; 2000US-0192099.
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PR PR 29-MAR-2000; 2000US-0193480.
```

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PR PR 15-MAY-2000; 2000US-0205230.
```

```
PR PR 09-JUN-2000; 2000US-0211315.
```

```
PR PR 25-JUL-2000; 2000US-0220534.
```

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XX PP
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```
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
```

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XX PI
```

```
PJ PJ Lillie J, Xu Y, Wang Y, Steinmann K;
```

```
XX PS WPI: 2001-451856/48.
```

```
DR DR
```

```
PP New peptide useful as a marker for the diagnosis of breast cancer -
```

```
PS Claim 1; Page 2912-2913; 3695pp; English.
```

```
CC CC The invention relates to human breast cancer expressed polynucleotides  
CC CC (AAU07544-AAU26789) and methods of assessing whether a patient is  
CC CC afflicted with breast cancer by examining the correlation between the  
CC CC expression of certain markers and the cancerous state of breast cells.  
CC CC The polynucleotides and encoded peptides are potential markers for  
CC CC detecting, diagnosing, monitoring, characterizing treating and  
CC CC potentially preventing breast cancer. The polynucleotides and encoded  
CC CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.
```

```
SQ SX Sequence 758 BP; 39 A; 300 C; 260 G; 154 T; 5 other;
```

```
SX SX
```

```
Query Match 27.6%; Score 74.4; DB 22; Length 758;  
Best local similarity 70.6% Pred. No. 0.00038;  
Matches 96; Conservative 0; Mismatches 40; Indels 0; Gaps 0.
```

```
OY QY 7 TTTTTCCTTTTTTTTTTTTTTTTTTCCCTTTTATTTTTTTTTTTT 66  
| | | | | | | | | | | | | | | | | | | | | |  
DB D1 TTTTTCCTTTTTTTTTTTTTTTTTTCTTTTATTGCGGGAGC 120  
| | | | | | | | | | | | | | | | | | | | | |  
OY QY 67 TTTTTCCTCCCCGTGCACACGTCATTTTGCGGCCACTCCC GGAGC 126  
| | | | | | | | | | | | | | | | | | | | | |  
DB D1 TTTTTCCTTTTTTNNAACCCCAACCAGATAATTTTGGGCCCCCCCCCTCTGGGGG 180  
| | | | | | | | | | | | | | | | | | | | | |  
OY QY 127 AGGGCGGGAGGGG 142  
| | | | | | | | | | | | | | | | | | | | | |  
DB D1 GCCCCCCCGGGGGG 196  
| | | | | | | | | | | | | | | | | | | | | |
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```
RESULT 14  
AAC77625/c ID AAC77625 standard; cDNA: 1355 BP.  
XX AC AAC77625:  
XX DT 08-FEB-2001 (first entry)  
XX DE Human cancer associated gene sequence SEQ ID NO:19.  
XX XX  
Human; cancer associated gene; cancer antigen; detection; cancer;  
diagnosis; cytosolic; proliferative; vulnerable; immunomodulator;  
antidiabetic; antisthmiaic; antiarthritis; antiviral;  
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
vasotropis; antipsoriatic; angiogenic; gene therapy; inflammation;  
immune disorder; haematopoietic cell disorder; autoimmune disorder;  
allergic reaction; graft versus host disease; organ rejection;  
hemostatic; thrombolytic; cardiovascular disorder; infection;
```

neurological disease; drug screening; ss.

Homo sapiens.
MO200055350-A1.
21-SEP-2000.
08-MAR-2000; 2000WO-USO5882.
12-MAR-1999; 99US-0124270.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM;
WPI; 2000-587533/55.
P-PSDB; AAB43416.

Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -

Claim 1; Page 625; 2352pp; English.

AAC77607 to AAC78448 encode the human cancer associated proteins given in ABA43398 to ABA44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antistaphmatic; antirheumatic; antiarthritic; antiinflammatory; antihypertoid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiac; thrombolytic; coagulant; neotropic; vasotropic; antiproliferative and angiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and ABA44240 represent sequences used in the exemplification of the present invention.

Sequence 1355 BP; 344 A; 398 C; 312 G; 298 T; 3 other;

Query Match 27.5%; Score 74.2; DB 21; Length 1355;
Best Local Similarity 86.3%; Pred. No. 0.00041;
Matches 82; Conservative 0; Mismatches 13; Indels 0; Gaps 0.

Y 7 TTTTTCCTTTTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTTTTAATTTTTTTTTT 66
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
D 1343 TTTTTCCTTT 1284
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Y 67 TTTTTCCTCCCCCGTGAGGAGCACAGCGTCAATT 101
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
D 1283 TTTTTCCTTTTTTTCAGTGGGAGACCACGTTTATT 1249
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
AA181299/c
ID AA181299 standard; cDNA: 377 BP.
XX AA181299;
DT 06-NOV-2001 (first entry)
XX Human polynucleotide SEQ ID NO 1359.
DE Human cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;

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```

? APPLICANT: Grandearl, Andrew David John
? TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
? TITLE OF INVENTION: MOLECULES
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Fish & Richardson P.C.
? STREET: 225 Franklin Street
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02110-2804
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: Windows 95
? SOFTWARE: FASTED for Windows Version 2.0b
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/964,127
? FILING DATE: 06-NOV-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Crews, Ph.D., L. Lee
? REGISTRATION NUMBER: P-43,567
? REFERENCE/DOCKET NUMBER: 07334/038001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617/542-5070
? TELEFAX: 617/542-8906
? TELEX: 200154
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1411 base pairs
? type: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: Coding Sequence
? LOCATION: 1...966
? US-08-964-127-5
?
? Query Match 25.7%; Score 69.4; DB 4; length 1411;
? Best Local Similarity 83.2%; Pred. No. 8.4e-06;
? Matches 79; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
?
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? US-09-496-692-5/c
? : Sequence 5, Application US/09496692
? : Patent No. 6313271
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? GENERAL INFORMATION:
? APPLICANT: Grandearl, Andrew David John
? TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
? TITLE OF INVENTION: MOLECULES
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Fish & Richardson P.C.
? STREET: 225 Franklin Street
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02110-2804
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,692
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/964,127
FILING DATE: 06-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...966
US-09-496-692-5

Query Match      25.7%: SCORE 69.4: DB 4: Length 1411:
Best Local Similarity 83.2%: Pred.No. 8.4e-06:
Matches 79: Conservative 0; Mismatches 16; Indels 0; Gaps 0.

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OY 67 TTTTTCCTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTAAATTTTTTTTTTTT 101
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RESULT 8
US-09-152-060-26/c
Sequence 26, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118

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OY **7**

RESULT 11

US-09-073-569-1/c

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? Sequence 1 Application US/09073569
? Patent No. 6084088
? GENERAL INFORMATION:
? APPLICANT: Sheppard, Paul O.
? APPLICANT: Grossmann, Angelika
? TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
? NUMBER OF SEQUENCES: 15
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Zymogenetics, Inc.
? STREET: 1201 Eastlake Avenue East
? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98102
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/073.569
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Sawislak, Deborah A
? REGISTRATION NUMBER: 37,438
? REFERENCE/DOCKET NUMBER: 97-14
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-442-6672
? TELEFAX: 206-442-6678
? TELEX:
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1733 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: Coding Sequence
? LOCATION: 34..1344
? OTHER INFORMATION:
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? US-09-073-569-1
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? Query Match 25.5%; Score 68.8; DB 3; Length 1733;
? Best Local Similarity 82.3%; Pred. NO.1.le-05;
? Matches 79; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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? QY 7 TTTTTCCTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTTTTAATTTTTTTTTTTT 66
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? QY 67 TTTTTCCTCCCCCGTGAGACACGCGTCAATT 102
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COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,918C
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/697,766
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: NMI-007CPDVZCPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 569..1616
US-08-955-918C-1

Query Match      25.5%; Score 68.8; DB 4; Length 2184;
Best Local Similarity 74.6%; Pred. No. 1,2e+05;
Matches 85; Conservative 1; Mismatches 28; Indels 0; Gaps 0;

QY   7 TTTTITTTTTTTTTTTTTTTTTTTTTTCCCTTTTTTTTTTTTTTTAAATTTTTTTTTT 66
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RESULT 13
US-08-697-766A-1/C
Sequence 1, Application US/08697766A
Patent No. 6399760
GENERAL INFORMATION:
APPLICANT: Gimeno, Carlos; Kieyn, Patrick; and Moore, Karen J.
TITLE OF INVENTION: RP Compositions and Therapeutic and
TITLE OF INVENTION: Diagnostic Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//08/697,766A
FILING DATE: 29-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

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6	73.8	27.3	485	9	US-10-063-547-43		Sequence 43, App1
7	73.8	27.3	485	9	US-09-989-735-245		Sequence 245, App1
8	73.8	27.3	485	9	US-09-990-444-245		Sequence 245, App1
9	73.8	27.3	485	9	US-09-989-730-245		Sequence 245, App1
10	73.8	27.3	485	9	US-09-990-436-245		Sequence 245, App1
11	73.8	27.3	485	9	US-09-991-181-245		Sequence 245, App1
12	73.8	27.3	485	9	US-09-993-687-245		Sequence 245, App1
13	73.8	27.3	485	9	US-09-989-734-245		Sequence 245, App1
14	73.8	27.3	485	9	US-09-997-653-245		Sequence 245, App1
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18	73.8	27.3	485	9	US-10-175-727-185		Sequence 185, App1
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ALIGNMENTS

RESULT 1
US-09-823-101-13

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Sequence 13, Application US/09823101
Patent No. US20020068307A1
GENERAL INFORMATION:
APPLICANT: Pluta, Jason
APPLICANT: Chen, Sei-Yu
APPLICANT: Hu, Ping
APPLICANT: Recipon, Hervé
APPLICANT: MacIha, Roberto
TITLE OF INVENTION: Compositions and Methods for Diagnosing, Monitoring
TITLE OF INVENTION: Staging, Imaging, and Treating Stomach Cancer
FILE REFERENCE: DEX-0205
CURRENT APPLICATION NUMBER: US/09/823,101
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/193,095
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 270
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (266)
NAME/KEY: unsure
LOCATION: (270)
US-09-823-101-13

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Query Match 99.3%; Score 268; DB 10; Length 270;

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Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Prior Filing Date: 1998-02-25	Prior Application Number: 60/078910
Prior Filing Date: 1998-03-20	Prior Application Number: 60/083322
Prior Filing Date: 1998-04-28	Prior Application Number: 60/084600
Prior Filing Date: 1998-05-07	Prior Application Number: 60/087106
Prior Filing Date: 1998-05-28	Prior Application Number: 60/087607
Prior Filing Date: 1998-06-02	Prior Application Number: 60/087609
Prior Filing Date: 1998-06-02	Prior Application Number: 60/087759
Prior Filing Date: 1998-06-02	Prior Application Number: 60/087827
Prior Filing Date: 1998-06-03	Prior Application Number: 60/088021
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088025
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088026
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088028
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088029
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088030
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088033
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088326
Prior Filing Date: 1998-06-04	Prior Application Number: 60/088167
Prior Filing Date: 1998-06-05	Prior Application Number: 60/088202
Prior Filing Date: 1998-06-05	Prior Application Number: 60/088212
Prior Filing Date: 1998-06-05	Prior Application Number: 60/088217
Prior Filing Date: 1998-06-05	Prior Application Number: 60/088555
Prior Filing Date: 1998-06-09	Prior Application Number: 60/08734
Prior Filing Date: 1998-06-10	Prior Application Number: 60/08738
Prior Filing Date: 1998-06-10	Prior Application Number: 60/08742
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Prior Filing Date: 1998-06-10	Prior Application Number: 60/08824
Prior Filing Date: 1998-06-10	Prior Application Number: 60/08826
Prior Filing Date: 1998-06-10	Prior Application Number: 60/08858
Prior Filing Date: 1998-06-11	Prior Application Number: 60/08861
Prior Filing Date: 1998-06-11	Prior Application Number: 60/08876
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Prior Filing Date: 1998-06-12	Prior Application Number: 60/089440
Prior Filing Date: 1998-06-16	Prior Application Number: 60/089512
Prior Filing Date: 1998-06-16	Prior Application Number: 60/089514
Prior Filing Date: 1998-06-16	Prior Application Number: 60/089532
Prior Filing Date: 1998-06-17	Prior Application Number: 60/089538
Prior Filing Date: 1998-06-17	

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15	PRIOR APPLICATION NUMBER: 60/089947
16	PRIOR FILING DATE: 1998-06-19
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19	PRIOR APPLICATION NUMBER: 60/089952
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32	PRIOR FILING DATE: 1998-06-24
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63	PRIOR APPLICATION NUMBER: 60/090682
64	PRIOR FILING DATE: 1998-06-26
65	PRIOR APPLICATION NUMBER: 60/090683
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67	PRIOR APPLICATION NUMBER: 60/091360
68	PRIOR FILING DATE: 1998-07-01
69	PRIOR APPLICATION NUMBER: 60/091478
70	PRIOR FILING DATE: 1998-07-02
71	PRIOR APPLICATION NUMBER: 60/091544
72	PRIOR FILING DATE: 1998-07-01
73	PRIOR APPLICATION NUMBER: 60/091519

RESULT 7
US-09-989-735-245/c
Sequence 245, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botsstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
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PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
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PRIOR FILING DATE: 1998-06-09
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090349

[illegible]

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3      : Sequence 245, Application US/09990444
4      : Publication No. US20020193300A1
5      : GENERAL INFORMATION:
6      :   APPLICANT: Askenazi, Avi J.
7      :   APPLICANT: Baker, Kevin P.
8      :   APPLICANT: Botstein, David
9      :   APPLICANT: Desnoyers, Luc
10     :   APPLICANT: Eaton, Dan L.
11     :   APPLICANT: Ferrara, Napoleone
12     :   APPLICANT: Fonzy, Sherman
13     :   APPLICANT: Gerber, Hanspeter
14     :   APPLICANT: Gerritsen, Mary E.
15     :   APPLICANT: Goddard, Audrey
16     :   APPLICANT: Grimaldi, J. Christopher
17     :   APPLICANT: Gurney, Austin L.
18     :   APPLICANT: Kijavlin, Ivar J.
19     :   APPLICANT: Napier, Mary A.
20     :   APPLICANT: Pan, James
21     :   APPLICANT: Paoni, Nicholas F.
22     :   APPLICANT: Roy, Margaret Ann
23     :   APPLICANT: Stewart, Timothy A.
24     :   APPLICANT: Tumas, Daniel
25     :   APPLICANT: Watanabe, Colin K.
26     :   APPLICANT: Williams, P. Mickey
27     :   APPLICANT: Wood, William I.
28     :   APPLICANT: Zhang, Zemin
29     :   TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
30     :   TITLE OR INVENTION: Acids Encoding the Same
31     :   FILE REFERENCE: P2730PIC19
32     :   CURRENT APPLICATION NUMBER: US/09/990,444
33     :   CURRENT FILING DATE: 2001-11-14
34     :   PRIOR APPLICATION NUMBER: 60/049787
35     :   PRIOR FILING DATE: 1997-06-16
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37     :   PRIOR FILING DATE: 1997-10-17
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44     :   PRIOR APPLICATION NUMBER: 60/075945
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59     :   PRIOR FILING DATE: 1998-06-02
60     :   PRIOR APPLICATION NUMBER: 60/087827
61     :   PRIOR FILING DATE: 1998-06-03
62     :   PRIOR APPLICATION NUMBER: 60/088021
63     :   PRIOR FILING DATE: 1998-06-04
64     :   PRIOR APPLICATION NUMBER: 60/088025
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66     :   PRIOR APPLICATION NUMBER: 60/088026
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Best Local Similarity 66.3%; Pred. No. 0.00019;
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Dy       461  TTTTTCCTTTTTTTTTTTTTTTCCCTTTTTTTTTTTAAATTTTTTTTTT
QY       67   TTTTTCCTCCCCTGGAGACACGTCATTGTGGGCCAGGTCCCGGGAGC
Db       401  TTTTTCCTGGAAAACAAGAACCAGCATTTATTCAGACTAATGTCTGGGCAGC
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DB 341 AGGAATAAATAGGAAGGAGGACGGGCGCAGGCC 305

RESULT 9

US-09-989-730-245/C

Sequence 245, Application US/09989730

Publication NO. US20020197674A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E..
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaeriv, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989,730
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4	PRIOR FILING DATE: 1998-06-23
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60	PRIOR FILING DATE: 1998-07-09

Query Match	27.38;	Score 73.8;	DB 9;	Length 485;
Best Local Similarity	66.98;	Pred. No. 0.00019;		
Matches 105; Conservative	0;	Mismatches 52;	Indels 0;	Gaps 0;

[illegible]

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US-09-991-181-245/C
Sequence 245, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
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PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR APPLICATION NUMBER: 60/088028
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090252

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RESULT 12
US-09-993-687-245/c
Sequence 245, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607

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RESULT 12	US-09-993-687-245/c
Sequence 245	Application US/09993687
Publication No.	US20020198149A1
GENERAL INFORMATION:	
APPLICANT:	Ashkenazi, Avi J.
APPLICANT:	Baker, Kevin P.
APPLICANT:	Bolstein, David
APPLICANT:	Desnoyers, Luc
APPLICANT:	Eaton, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Fong, Sherman
APPLICANT:	Geber, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Klavin, Ivar J.
APPLICANT:	Napier, Mary A.
APPLICANT:	Pan, James
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunnes, Daniel
APPLICANT:	Watanabe, Colin K.
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William I.
APPLICANT:	Zhang, Zemin
TITLE OR INVENTION:	Secreted and Transmembrane
TITLE OR INVENTION:	Acids Encoding the Same
FILE REFERENCE:	P2730P1C11
CURRENT APPLICATION NUMBER:	US/09/993, 687
CURRENT FILING DATE:	2002-11-14
PRIOR APPLICATION NUMBER:	60/049787
PRIOR FILING DATE:	1997-06-16
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PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087759

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 9 PRIOR APPLICATION NUMBER: 60/088025
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PRIOR FILING DATE:	1998-06-22

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62	PRIOR FILING DATE: 1998-07-09

Query Match	27.3%;	Score 73.8;	DB 9;	Length 485;
Best Local Similarity	66.9%;	Pred. No. 0.00019;		
Matches 105;	Conservative 0;	Mismatches 52;	Indels 0;	Gaps 0;

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RESULT 13
US-09-989-734-245/c
; Sequence 245, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC64
; CURRENT APPLICATION NUMBER: US/09/989,734
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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58	PRIOR APPLICATION NUMBER: 60/091978
59	PRIOR FILING DATE: 1998-07-07
60	PRIOR APPLICATION NUMBER: 60/091982
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63	PRIOR FILING DATE: 1998-07-09

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RESULT 14
US-09-997-653--245/c
: Sequence 245, Application US/09997653
: Publication No. US20030008297A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertlisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavini, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Matanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PIC38
: CURRENT APPLICATION NUMBER: US/09/997,653
: CURRENT FILING DATE: 2001-11-15
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
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: PRIOR FILING DATE: 1998-03-20
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: PRIOR FILING DATE: 1998-04-28
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: PRIOR FILING DATE: 1998-06-02
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: PRIOR APPLICATION NUMBER: 60/087827
: PRIOR FILING DATE: 1998-06-03
: PRIOR APPLICATION NUMBER: 60/088021
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088025

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17	PRIOR APPLICATION NUMBER: 60/090444
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19	PRIOR APPLICATION NUMBER: 60/090445
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21	PRIOR APPLICATION NUMBER: 60/090472
22	PRIOR FILING DATE: 1998-06-24
23	PRIOR APPLICATION NUMBER: 60/090535
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51	PRIOR APPLICATION NUMBER: 60/091544
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54	PRIOR FILING DATE: 1998-07-02
55	PRIOR APPLICATION NUMBER: 60/091626
56	PRIOR FILING DATE: 1998-07-02
57	PRIOR APPLICATION NUMBER: 60/091633
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091978
60	PRIOR FILING DATE: 1998-07-07
61	PRIOR APPLICATION NUMBER: 60/091982
62	PRIOR FILING DATE: 1998-07-07
63	PRIOR APPLICATION NUMBER: 60/092182
64	PRIOR FILING DATE: 1998-07-09

Query Match	27.38;	Score 73.8;	DB 9;	Length 485;
Best Local Similarity	66.98;	Pred. No. 0.00019;		
Matches 105; Conservative	0;	Mismatches 52;	Indels 0;	Gaps 0;

[illegible]

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QY 67 TTTTTCCTCCCGTGGGAGCACAGTTCATTTGGGGCCAGCTCTCCCGGGAGC 126
    |||||
DB 401 TTTTTCCTCCCGTGGGAGCACAGTTCATTTGGGGCCAGCTCTCCCGGGAGC 342
QY 127 AGCGCGCGGAGGGGGGTGGAGCAGGGGCAAGC 163
    |||
DB 341 AGCAATTAATTAAGGAAGGAGGGGAGGGGCGAGGGC 305

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RESULT 15

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US-10-174-590-185/c
; Sequence 185, Application US/10174590
; Publication NO. US20030008352A1
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 185
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-185

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Query Match 27.3%; Score 73.8; DB 9; Length 485;

Best Local Similarity 66.9%; Pred. No. 0.00019;

Matches 105; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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    |||||
DB 461 TTTTTCCTCCCGTGGGAGCACAGTTCATTTGGGGCCAGCTCTCCCGGGAGC 402
QY 67 TTTTTCCTCCCGTGGGAGCACAGTTCATTTGGGGCCAGCTCTCCCGGGAGC 126
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DB 401 TTTTTCCTCCCGTGGGAGCACAGTTCATTTGGGGCCAGCTCTCCCGGGAGC 342
QY 127 AGCGCGCGGAGGGGGGTGGAGCAGGGGCAAGC 163
    |||
DB 341 AGCAATTAATTAAGGAAGGAGGGGAGGGGCGAGGGC 305

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Search completed: March 22, 2003, 00:22:06
 Job time : 62.7109 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2003, 16:21:58 ; Search time 1299.33 Seconds
(without alignments)
3365.420 Million cell updates/sec

Title: US-09-823-101-13

Perfect score: 270
Sequence: 1 acaagctttttttttttt.....taaacagacaagcaantctn 270

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hlc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hlc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91.6	33.9	361	9	AI819970 wj88h03.x
2	90.8	33.6	400	9	AL513741
3	89.6	33.2	443	14	BO637878
4	89.2	33.0	1859	12	BF128527
5	89	33.0	307	9	AL513839
6	89	33.0	315	9	AL513829

7	89	33.0	951	17	A2672893	A2672893 ENTJ74TF
8	88.2	32.7	328	9	AI869367	AI869367 t39904. x
9	87.8	32.5	229	9	AL515163	AL515163
10	86.8	32.1	339	9	AL515041	AL515041
11	86.6	32.1	851	9	AL514003	AL514003
12	86	31.9	1291	14	BQ218448	BQ218448 AGENCOURT
13	85.6	31.7	235	13	BG991112	BG991112 MR2-HT118
14	85.6	31.7	399	9	AL514193	AL514193
15	85.4	31.6	242	9	AI383919	AI383919 tc99h01. x
16	84.8	31.4	608	14	BO747550	BO747550 UT-N-FAO-
17	83.6	31.0	368	9	AI302910	AI302910 q04h12. x
18	83.4	30.9	1077	14	BM907650	BM907650 AGENCOURT
19	83.2	30.8	206	9	AI537515	AI537515 tP04e04. x
20	83.2	30.8	288	9	AI439443	AI439443 tJ04e11. x
21	83	30.7	556	14	BO746926	BO746926 UT-N-FAO-
22	82.8	30.7	445	9	AL514067	AL514067
23	82.8	30.7	904	12	BE972180	BE972180 601651743
24	82.8	30.7	913	17	BH154234	BH154234 ENTTH85TF
25	82.6	30.6	928	13	BM415733	BM415733 OP20814 M
26	82.2	30.4	244	13	BI001693	BI001693 MR3-HN014
27	82.2	30.4	363	13	BM087984	BM087984 501324 MA
28	82	30.4	636	14	BO746698	BO746698 UT-N-FAO-
29	81.8	30.3	563	9	AI687415	AI687415 tP95g09. x
30	81.8	30.3	987	12	BE965129	BE965129 601658922
31	81.6	30.2	710	12	BE971954	BE971954 601651194
32	81.6	30.2	727	9	AI924923	AI924923 wN25g09. x
33	81.6	30.2	940	12	BE963809	BE963809 601657460
34	81.4	30.1	300	9	AI625329	AI625329 tS21f11. x
35	81.4	30.1	890	9	AL513985	AL513985
36	81.2	30.1	549	9	AI679631	AI679631 tU75f10. x
37	81.2	30.1	713	13	BI521708	BI521708 603081645
38	81	30.0	400	9	AI588189	AI588189 tB97g03. x
39	80.8	29.9	269	9	AI583054	AI583054 tS03g06. x
40	80.8	29.9	754	17	CNS072NG	AL426434 clone BAO
41	80.8	29.9	961	12	BG255742	BG255742 602368213
42	80.6	29.9	226	10	AM081797	AM081797 xB55a05. x
43	80.6	29.9	291	9	AI919506	AI919506 tP22b12. x
44	80.6	29.9	337	9	AI662880	AI662880 wJ97h05. x
45	80.6	29.9	1002	12	BE963758	BE963758 601657405

ALIGNMENTS

RESULT 1
LOCUS AI819970 361 bp mRNA linear EST 21-DEC-1999
DEFINITION wj88h03.x1 NCI-CCAP_Lym12 Homo sapiens cDNA clone IMAGE:240941 3'
similar to contains element MSRI repetitive element ;, mRNA
sequence.
ACCESSION AI819970
VERSION AI819970.1 GI:5439049
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 361)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/nclogap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: ccgaps-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bhrp/image/image.html
Insert Length: 4826 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 354.
Location/Qualifiers

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1. .361
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/db_xref="taxon:9606"
/clone="IMAGE:240941"
/clone_11b="NCI-CGAP_Lym12"
/tissue_type="lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/note="organ: lymph node; Vector: pCMV-Sport6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: 019g df. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

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ORIGIN

Query Match      33.9%; Score 91.6; DB 9; Length 361;
Best Local Similarity 65.8%; Pred. No. 0.0099;
Matches 133; Conservative 0; Mismatches 69; Indels 0; Gaps 0

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41 TTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTT 100
|||||
67 TTTTTTTTTTCCCTGGAGACACACGCTCAATTTGGGGCCAGTCTCCGGGGAGC 126
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101 TTTTTTTTCCCCCAACAGGGGGGCAAGGGGTGTGGGCCCCCCCCCCACCCCG 160
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127 AGGCCCGGAGGGGGGGTGCAGCAGGGGCAACGCCCCAGACGCGGGCCACAC 186
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161 GGGGGGGGGGAGGGGGGGGAAACCCGAAACCCCGGCGCAAGGGGGGGGGG 220
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187 AGGCACAAAGGGTGGGTCCCG 208
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221 GGGCCACAAACAAATGTTCCG 242

RESULT 2
AL513741
LOCUS
DEFINITION
AL513741 LTI_NFL006.Pl2 Homo sapiens cDNA clone CLOBA0082F03 3
prime, mRNA sequence.
AL513741
ACCESSION
VERSION
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 400)
I.I.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .400
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBA0082F03"
/clone_11b="LTI_NFL006.Pl2"
/tissue_type="Placenta"
/note="Vector: pCMV-Sport 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"
FEATURES
SOURCE

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[illegible]

VERSION	AI869367.1	GI:5543335
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: c9apbs@email.nih.gov Tissue Procurement: Christopher Moskaluk, N.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www-bio.lnl.nhl.gov/bbrp/image/image.html Insert length: 1003 Std Error: 0.00 Seq primer: -40UP from Gdbco High quality sequence stop: 216. Location/Qualifiers	
FEATURES	1..229	
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Matches 117; Conservative	0; Mismatches 48; Indels 0; Gaps 0;	
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Dd	46 TTTTTCCTTTTTTTTTTTTTTTTCTTTTTTTTTTTTCTTTTTTTTTTTT 105	
Oy	67 TTTTTCCTTCCTCCCGTGAGACACAGCGCAATTGGGGGCCACGTCCCGGGGAGC 126	
Dd	106 TTTTTCCTTTTCCCCCGGGAACAACCTTTTTCCTTTTAAAGGGGGAATAACCCCGGGGG 165	
Oy	127 AGGGCGGGAGGGGGGTGTGAGCAGGAGGCACGCCCGAAGA 171	
Dd	166 GGGGGGGGGAAGAGGGGGGGGGCCCCCCCCCCCANAANA 210	
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DEFINITION	AL515163 LTI.NFL006.PL2 Homo sapiens cdna clone CLOBB022ZF05 3 prime, mRNA sequence.	
ACCESSION	AL515163	
VERSION	AL515163.1 GI:12778656	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.	
TITLE	Full-length CDNA libraries and normalization	
JOURNAL	Unpublished (2001)	

[illegible]

Db	111	TTTTTTTGGCCCCACAGAGGGGGGTTTTTTTTTAAATGTGGGAATTTCCCCGGGGAAAG	170
OY	127	AGGGCGCGGGAGAGGGGGGTGTGACAGAGGGGCAACCCCCAGAAACGGGGGCGACACAC	186
Db	171	GCTAAAGAGGGGGGGGGGGGTGTAAAGGAAACCCCGCTTCGGTTTTTCCCCCCCC	230
OY	187	AGGCACCAAA	196
Db	231	AGGGGAAAAA	240
RESULT 13			
LOCUS	BG991112	235 bp	mRNA linear
DEFINITION	MR-H1189-270101-001-d04 HT1189 Homo sapiens cDNA, mRNA sequence.		EST 13-JUN-2001
ACCESSION	BG991112		
VERSION	BG991112.1	GI:14395182	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 235) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunslein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496 (2000)
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G.		

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/ICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR2&t2=MR2-HT1189)
270101-001-d04&t3=2001-01-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 39
High quality sequence stop: 254.

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            Site.2: Sma1; A mini-library was made by cloning products
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            No. 196,716 - Ludwig Institute for Cancer Research)
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ORIGIN
Query Match      31.7%; Score 85.6; DB 13; Length 235;
Best Local Similarity 70.1%; Pred. No. 0.074;
Matches 115; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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[illegible]

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/note="Vector: pcMVSPORT 6; site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT      57 a      135 c      60 g      120 t      27 others
ORIGIN
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Best Local Similarity 61.1%; Pred. No. 0.045;
Matches 116; Conservative 12; Mismatches 62; Indels 0; Gaps 0;

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Oy   67 TTTTTCCTTTTCCCCCGTGAGACACGTCATTGTGGGGGCCAGTCTCCC GGGGAGC 126
    Db 119 TTTTTCCTTTTCCCCCGTGAGACACGTCATTGTGGGGGCCAGTCTCCC GGGGAGC 178

Oy   127 AGGGCGGGGAGGGGGGGTGGAGACAGGGGGCAACGCCCCACAGAACCGCGGGCGACACAC 186
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Oy   187 AGGCACAATA 196
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				EST 28-MAR-1999

